

## **FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGCTGGTAAGGATTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTGTGAAGTTGTAACAGAAAACCTGTTAGAAATGTGGTGGT  
TTCAGCAAGGCCTCAGTTCCCTTCAGCCCTTGTAAATTGGACATCTGCTGCTTCAATT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTACCTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTGGGCAATGCTAAATATTGCGGCAGTTATGCATTG  
CTACCATTTATGTTGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA  
TTAAACAAAGGCTGGCCTTGTACTTGAATACTGAGTTGTTAGGACTTCTATTGGCAAACCTT  
CCAGAAAAACAACCCCTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTGGTATGGCCTCAT  
TATATATGTTGTTAGACCATCCTTCTACCAAATGCAGCCAAAATCCATGGCAAACAAGTC  
TTCTGGATCAGACTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTAGCATGCTGACTTGCTC  
ATCAGTTGTCACAGTGGCAATTGGGACTGATTAGAACAGAAACTCCATTGGAACCCCGAGG  
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGCTATGCTATTCCCTTCTT  
GGTTTTCTGACTTACATTGCTGATTTCTGAAACCTTACGGGTGGAAGCCAATTACA  
TGGATTAACCCCTATGACACTGCACCTGCCCTATTACAATGAACGAACACGGCTACTTCCA  
GAGATATTTGATGAAAGGATAAAATATTCTGTAATGATTGATTCTCAGGGATTGGGAAAGG  
TTCACAGAAGTTGCTTATTCTCTGAAATTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTATCTCAGAAAATAAGTCAAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIYVRYKQVHALSPEENVIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG  
MGSLYMFVQTILSYQMOPKIHGKQVFIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

**Important features:**

**Type II transmembrane domain:**

amino acids 13-33

**Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

**N-myristylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### **FIGURE 3**

CGGACGGCGTGGCGGACCGTGGGGAGAGCCGAGTCCCGCTGCAGCACCTGGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGTGGCCCCAGCGTGTGGCCTCGGGAGTGGGAAGTGGAGGCAGGAGCCTTC  
CTTACACTCGCCATGAGTTCCATCGACTCCAGCATGATTACCTCCAGATACTATTTTG  
GATTGGGTGGCTTCTTCATGCGCAATTGTTAAAGACTATGAGATACTGTCAGTATGTTGTACAG  
GTGATCTCTCCGTGACGTTGCATTTCATGCACCATGTTGAGCTCATCATCTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCGTTATTTCACTGGAAATGAACCTGTGTGTAATTCTGCTGATCCTGG  
TTTCATGGTGCCTTTTACATTGGCTATTTATTGTGAGCAATATCGACTACTGCATAAACAGA  
CTGCTTTCTGCTCTATGGCTGACCTTATGTTCTGAAACTAGGAGATCCCTTCC  
CATTCTAGCCAAAACATGGATCTTATCCATAGAACAGCTCATCAGCGGGTTGGTGTGATTGGAG  
TGACTCTCATGGCTCTTCTGGATTGGTGTCACTGCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAAGAAAAAGAAAAGGATGCAATGGCACGGAGAACATGTTCCAGAAGGGGAAGTGCATAACA  
AACCATCAGGTTCTGGGAATGATAAAAAGTGTACCTCAGCATCAGGAAGTGAATCTTACT  
CTTATTCAACAGGAAGTGGATGCTTGGAAAGAATTAAGCAGGCGACTTTCTGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAAATACTCCAAAACCTCAAGGGAAATATTTAATTTCCTGGTT  
ACTTTTCTCTATTACTGTGTTGGAAAATTTCATGGTACCATCATATTGTTTGATCGAGTT  
GGGAAAACGGATCTGTACAAGAGGCATTGAGATCACTGTGAATTATCTGGAAATCCAATTGATGT  
GAAGTTTGGTCCAACACATTCTTCATTCTGTTGAAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTTACCAAGTCTTTATGCATCTCTAGCAACTGCTCCATGTCATTGCTCTG  
CTATTAGCACAGATAATGGCATGTACTTGTCTCTGTGCTGATCCGAATGAGTATGCCTT  
AGAATACCGCACCATAACTGAAGTCCTGGAGAACTGCAGTTCAACTCTATCACCGTTGGTTG  
ATGTGATCTCCTGGTCAGCGCTCTCTAGCATACTCTCCCTATTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTCAAAATTAA  
GATATAAGAGGGGGAAAATGGAACCAGGGCTGACATTATAAACAAACAAAATGCTATGGTAGC  
ATTTCACCTTCATAGCATACTCTCCCTCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG  
AACATGAGAGGGAGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCGTGTGGATATGAGGCTGG  
TGTAGAGGCCAGAGGAGCAAGAAACTAAAGGTGAAAATACACTGGAACCTCTGGGGCAAGACATGT  
CTATGGTAGCTGAGCCAACACGTTAGGATTTCCGTTAAGGTTCACATGGAAAAGGTTATAGCTTGC  
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAAAAAAAAGGGCGGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTGGCCGCCATGGCCAACCTGTTATTGCAGCTTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQLFFFGFGWLFFMRQLFKDYEIRQYVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTMYFFWKLGDP  
FPILSPKHGILSIEQLISRVGVIGVTIMALLSGFGAVNCPTYMSYFLRNVTDILALERRLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSCFWGMIKSVTSASGSENLTLIQQEVDALEELSRQ  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLAQIMGMY  
FVSSVLLIRMSMPLLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

**Important features:**

**Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## **FIGURE 5**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC  
AGAACTCTCCATCCGGACTAGTTATTGAGCATTGCTCTCATATCACCAAGTGGCCATCTGAGGT  
GTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT  
TCCATCTGGACCACCGAGGCTCTGGTCCAAGGCTTTGCGTGCAGAAGAGCTTCCATCCAGGT  
GTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCAGCAGCTGAATTTCACAG  
AAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTGGCCGGCAAGGACCAAGTGAAACAGCC  
TTGAAAGCTAGCTTGAACACTTGCAGCTATGGCTGGGTGGAGATGGATTGCTGTATCTCTAG  
GATTAGCCCCAAACCCCAAGTGTGGGAAAATGGGGTGGGTGTCTGATTGGAAAGGTTCCAGTGA  
GCCGACAGTTGCAGCCTATTGTACAACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA  
ATTATCACCACCAAGATCCCATATTCAACACTCAAACCTGCAACACAAACACAGAATTATGT  
CAGTGACAGTACCTACTCGGTGGCATCCCCACTCTACAATACCTGCCCCTACTACTCCTC  
CTGCTCCAGCTTCACTTCTATTCCACGGAGAAAAAAATTGATTGTCACAGAAGTTTATG  
GAAACTAGCACCATGTCTACAGAAACTGAACCATTGTTGAAAATAAGCAGCATTCAAGAATGA  
AGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGCTCTCCTCTTGGTGTG  
CAGCTGGCTTGGATTTCGTATGTCAAAAGGTATGTGAAGGCCTTCCCTTACAAACAAGAAT  
CAGCAGAAGGAAATGTCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCATGATAGCAACCTAA  
TGAGGAATCAAAGAAAATGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGC  
GATGCTGGAGCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTT  
CATGCTCTTACCCGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAAGAAAGTCCA  
CCCTGGTTCTTAACCTGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAT  
GCCCTTCTCTTATGTAACCTGTCTGGATCCTATCTCTACCTCAAAGCTCCCACGGCT  
TTCTAGCCTGGCTATGCTTAATAATATCCACTGGAGAAAGGAGTTTGCAAAGTGCAAGGAC  
CTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGGTGGTTG  
AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGACCCCTTCTCA  
GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTCTGAGGCCGTAACGACAAAAGAAT  
GGCAGAAAAGTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTGTAAA  
GCTAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC  
ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGGTGGAACTACTGTTAGAACACACACA  
CTTACTTTCTGGCTCTACCACTGCTGATATTTCTCTAGGAATAACTTTACAAGTAACA  
AAAATAAAAATCTTATAAATTCTATTCTGAGTTACAGAAATGATTACTAAGGAAGATT  
ACTCAGTAATTGTTAAAATCAACAAACATTTGCTGAATAGCTACTATATGTC  
AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATTGAAATTATTCTCTAAAAAATTGCA  
AACATAGTACGCTTCTGATATTCTCTCTAATATGGCAACCATTATAACCTTAATT  
TTTATTCTGCTGAGACTAATCTTATTCTCTAATATGGCAACCATTATAACCTTAATT  
TATTATAACATACTAAGAAGTACATTGTTACCTCTATACCAAGCACATTAAAAGTGC  
ATTAACAAATGTACTAGCCCTCTTTCCAACAAAGAAGGGACTGAGAGATGCAGAAATATT  
TGTGACAAAAAATTAAAGCATTTAGAAAACCTT

## **FIGURE 6**

MARCFSLVLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACRLLG  
LSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYN  
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTPPAPASTSIPR  
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK  
RYVKAFFPTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 7

CGCCCGCCTCCGCACCCGCGGGCCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCCCGGC  
GGCCTCCCGCGGGAGCGAGCAGATCCAGTCGGGCCCGAGCGCAACTCGGTCCAGTCGGGGCG  
CGGCTCGGGCGCAGAGCGGAGATGCAGCGCTTGGGCCACCCCTGCTGTGCCTGCTGGCG  
CGGCGGTCCCCACGCCCGCGCCGCTCCGACGGCACCTCGGCTCCAGTCAGGCCGGCCCG  
GCTCTCAGTACCCGAGGAGGCCACCTCAATGAGATGTTCCGCAGGTTGAGGAACGTGAT  
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAATTCAAGATAACCAACAACCAGAC  
TGGACAAATGGTCTTCAGAGACAGTTACATCTGAGGAGACAAGAAGGGAGAAGGAGGCC  
ACGAGTCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTGCCAGCTCCAGTAC  
ACCTGCCAGCCATGCCGGGCCAGAGGATGCTCTGCACCCGGGACAGTGTGCTGTGGAGACCA  
GCTGTGTCTGGGGTCACTGCACCAAATGCCACAGGGGAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCCGGGCTGTGCTGTGCCCTCCAGAGAGGCTGCTGTCCCTGTGTC  
ACACCCCTGCCCGTGGAGGGCAGCTTGACATGACCCCGCCAGCCGGCTCTGGACCTCATCAC  
CTGGGAGCTAGAGCCTGATGGAGCCTGGACCGATGCCCTGTGCCAGTGGCCTCCCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGCAAGCCGACCTTCGTGGGAGCCGTGACCAAGATGG  
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCG  
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCCTGGGGAGCCCTGCCAG  
CCGCCGCTGCACTGCTGGAGGGAAAGAGATTAGATCTGGACCAGGCTGTGGTAGATGTGAA  
TAGAAATAGCTAATTATTCCCAAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTCTA  
CATCTCTCCCAGTAAGTTCCCTCTGGCTGACAGCATGAGGTGTTGCAATTGTCAGCT  
CCCCCAGGCTGTTCTCCAGGCTCACAGTCGGTCTGGGAGAGTCAGGCAGGTTAAACTGCA  
GGAGCAGTTGCCACCCCTGTCCAGATTATGGCTGCTTGCCCTACAGTTGGCAGACAGCG  
TTTGTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAACAAATGTGGAGTCTCCCT  
TGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAACACATCAACCTGGCAAAATG  
CAACAAATGAATTTCACGCAGTTCTTCATGGGCAAGGTAAGCTGTGCCTCAGCTGTG  
AGATGAAATGTTCTGTTCACCTGCATTACATGTGTTATTCACTCCAGCAGTGTGCTCAGCT  
TACCTCTGTGCCAGGGCAGCATTTCATATCAAGATCAATTCCCTCTCAGCACAGCCTGGGG  
AGGGGTCATTGTTCTCTGTCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTGCC  
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCATCTGGTGTGACTCTAAGCTAGTGC  
CTCCACTACCCCACACCAGCCTGGTGCACCAAAAGTGTCTCCCAAAAGGAAGGAGATGGGAT  
TTTCTGAGGCATGCACATCTGAATTAGTCAGGAAACTAATTCTCACATCCCTCTAAAGTAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCGCTCCCTCTAATGAAGACAATG  
ATTGACACTGCTCCCTCTGGCAGTTGCAAGTTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAACAGTACTTAGGTAATTGTAAGGGCGAGGATTATAATGAAATTG  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACAGTGGAGAAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGGTGTAAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATG  
TTTCAGGTGTCACTGGACTGTTGCCACCATGTATTCACTCCAGAGTTCTTAAAGTTAAAGTTGCA  
CATGATGTATAAGCATGTTCTTGAGTTAAATTATGTATAAACATAAGTTGCAATTAGAA  
ATCAAGCATAAAATCACTCAACTGCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLAAAVPTAPAPAPTATSAVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEAAAKASSEVNLANLPPSYHNETNTDKVGNNTIHVREIHKITNNQTGQMVFSE  
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQRMCLTRDSECCGDQLCVWGH  
TKMATRGSGNTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDG  
ALDRCPGASGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPDEYEVGSFMEEVHQELEDLE  
RSLTEEMALGEPAAAAALLGGEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 9**

CGGACGCGTGGCGGACGCGTGGGGCTGTGAGAAAGTCCAATAATACATCATGCAACCCAC  
GGCCCACCTTGTGAACTCCTCGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGTCTCAATCTGCAAATCTATGGGTCTGGGCTCTCTGGACCCCTT  
AACTGGGTACTGGCCCTGGCCAATGCGCTCGCTGGAGCCTTGCCTCCTACTGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTCCCCCTAATCTGCCTCATCCGACACTCCGTTACC  
ACACTGGGTCAATTGGCATTGGAGCCCTACCTGCACCCCTGTGCAGATAGCCCAGGTACATCTG  
GAGTATATTGACCACAAGCTAGAGGAGTGCAGAACCCGTAGCCCGCTGCATCATGTGCTTTT  
CAAGTGCCTGCCTCTGGTGTCTGGAAAAATTATCAAGTCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTCTGTGTCTAGCCAAAATGCGTCTGCTACTCATGCGAAC  
ATTGTCAAGGGTGGTCGTCCCTGGACAAAGTCACAGACCTGCTGCTGTTGGAAAGCTGCTGGT  
GGTCGGAGGCGTGGGGTCTGCTCTTTCTCCGGTCGACATCCGGGCTGGGTAAAG  
ACTTTAAGAGCCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCCTGGGGCCTAT  
GTCATGCCAGCGGCTTCTCAGCGTTTCCGGCATGTGTGTCGACACGCTCTCCCTGCTTCT  
GGAAGACCTGGAGCGAACACGGCTCCCTGGACCGGCCACTACATGTCCAAGAGCCTCTAA  
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGAACACAAGAAGAGGAAGTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCACCCACCGTCCAGCCATCCAACCTCACTTCGCTTACAGGT  
CTCCATTGTGGTAAAAAAAGTTTAGGCCAGGCGCCGTGGCTACGCCTGTAATCCAACACT  
TTGAGAGGCTGAGGCCGGGATCACCTGAGTCAGGAGTTGAGACCAGCCTGCCAACATGGT  
AAACCTCCGTCTTAAACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA  
GCTACTCGGAGGCTGAGGCAGGAGAACGCTGAAACCCGGAGGCAGAGGTTGCAAGGCCA  
GATCGGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAA  
AAGATTTATTAAAGATATTTGTTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLFWTL  
NWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVVLDKVTDLFFFGLKLLVVGGVGVLSSFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYMSKSLKILGKKNEAPPDNKKRKK

**Important features:**

**Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

**N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

**Hypothetical YBR002c family proteins.**

amino acids 276-288

**Ammonium transporters proteins.**

amino acids 204-231

**N-myristoylation sites.**

amino acids 60-66, 78-84

**Amidation site.**

amino acids 306-310

### **FIGURE 11**

GCCCCCGCCGCCGGCGCCGGCGCCCGAAGCCGGAGCCACCGCCATGGGGCCTGCCCTGGGAGGCCTGC  
TCCCTGCTCAGCTGCGCGTCTGCCCTGCCGCTCTGCCCTGCATCCTGTGCAGCTGCTGCCCGC  
CAGCCGCAACTCCACCGTGAGGCCCCTCATCTCAGCTCTGCCCTCTCCCTGGGGTGTGGTGTCCA  
TCATTATGCTGAGCCGGCGTGGAGAGTCAGCTTACAAGCTGCCCTGGGTGTGAGGAGGGGCC  
GGGATCCCCACCGTCTGCAGGGCACATCGACTGTGGCTCCCTGCTTGCTACCGCCTGTCTACCG  
CATGTGCTTCGCCACGGCGGCCCTCTTCTCTTCTTACCCCTGCTCATGCTCTGCGTGAGCAGCA  
GCCGGGACCCCCGGCTGCCATCCAGAATGGGTTTGGTTCTTAAGTCCTGATCCGGTGGGCC  
ACCGTGGGTGCCCTCATCCCTGACGGCTCCTCACCAACATCTGGTCTACTCCGGCTCGTGGG  
CTCCTCCTCTCATCCTCATCCAGCTGGCTGCTCATGACTTGCCACTCCTGAACCAGGGT  
GGCTGGCAAGGCCGAGGAGTGCGATTCCCGTGCCTGGTACGCAGGCCCTCTTCTTCTCACTCTCC  
TTCTACTTGCTGCGATCGCGCCGTGGCGTGATGGTCATGTACTACACTGAGGCCAGGGCTGCCA  
CGAGGGCAAGGTCTCATCAGCCTCAACCTCACCTCTGTGTCGTCCATCGTGTCCACTCCTGC  
CCAAGGTCCAGGACGCCAGCCAACTCGGGTCTGCTGCAGGCCCTCGGTCATCCACCCATG  
TTTGTCACCTGGTCAGCCCTATCCAGTATCCGAACAGAAATGCAACCCCATTGCCAACCCAG  
GGGCAACAGACAGTTGTGGCAGGGCCGGGCTTGAACACCCAGTGTGGGATGCCCCGAGAT  
TGGGCCTCATCATCTCCCTGTGCACCCTCTTCATCAGTCTGCGCTCCTCAGACCCACGG  
AACAGCCTGATGCAGACCCGAGGTGCCCACCTTATGCTAGACGCCAGGT  
GGCAGCCTGTGAGGCCGGCCTTGAACACCGAGCCAGGTGCACCTACAGCTACCCTTCTCC  
ACTTCTGCCCTGGTGTGCCCCTACTGCACGTCATGATCACCACCGGTGAG  
ACCCGGAAAGATGATCAGCACGTGGACGCCGTGTGGTGAAGATCTGTGCCAGCTGGCAGGGCTGCT  
CCTCTACCTGTGGACCCCTGGTAGCCCCACTCCCTGCCAACCCGCACTTCAGCTCGAGGCAGCCTCA  
CAGCCTGCCATCTGGTCCTCCGCACCTGGGTGCCTCCGGGTGACAGCCCACCTGCCCCTCC  
CCCACACCAAATCAGCCAGGTGAGCCCCACCCCTGCCCCACCGGGG  
CTTCTAGTCGTAGTGGCCTTCAGGGTCCGGAGGACATCAGGCCTCCTCGCAGGCCCCATCCCCCGGCCAC  
ACCCACACGGTGGAGGTGCCTTCCCCTCCCTCCCTGGGTGCCCCAACTTCAGCATCTGGATGA  
AGGGCTCCTTGTCCTCAGGGCTCCACGGGAGCGGGGCTGTGGAGAGGCGGGGAACTCCACAC  
TGGGGCATCGGCACTGAAGCCCTGGGTTTCCGTACGTCCCCAGGGGACCCTGCCCCCCTCCGT  
GACTTCGTGCCTTACTGAGTCTCAAAGACTTTCTTAAAAACAAGCCAGGTGCGTTAAAAAAA

## **FIGURE 12**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLFILQLVLLIDFAHAWNQRWLKGAE  
ECDSRAWYAGLFFFLLFYLLSIAAVALMFYYTEPSGCHEGKVFISLNLTFCVCVSIAAVLPKV  
QDAQPNGLLQASVITLYTMFVTVSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRAFDNEQDGVTYSY  
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICASWAGLLLWTLVAPLLRNDF  
FS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

## **FIGURE 13**

CGGGCCAGCCTGGGGCGGCCAGGAACCACCCGTTAAGGTGTCTCTTTAGGGATGGTGA  
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCAGGGATGAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCATGCTCTGCGCAATATCCATTCCATCAACCCCACACAA  
CTCATGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTGTTGTCACCTTGACCTCTTATTGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGGAGGTGATGCAGTATGACTACTATTCTTCATAT  
TTTGATATATTCTCTGGCAGTTTCGATTAAAGTGTAAACTTGCAATGCTGTGTCAG  
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTACTAGCAAAAG  
TGATCCTTCGAAGCTTCTCAAGGGCTTGGCTATGTGCTGCCATCATTCAATTCA  
CTTGCCTGGATTGAGACGTGGTCCCTGGATTCAAAGTGTACCTCAAGAACAGAAGAAA  
CAGACTCCTGATAGTTAGGATGCTTCAGAGAGGGCAGCACTTACCTGGTGGTCTTCTGATG  
GTCAGTTTATTCCCTCCTGAATCGAACAGGATCTGAAGAACAGTGAAGAAAACAGGACAGT  
GAGAAACCACTTAGAACTATGTACTACTTTGTTAAATGTGAAAAACCCCTCACAGAAAGTC  
ATCGAGGCAAAAGAGGCAGGCAGTGGAGTCCCTGTCGACAGTAAAGTTGAAATGGTACGTC  
CACTGCTGGCTTATTGAACAGCTAATAAGATTATTGTAAACCTCACAAACGTTGTAC  
CATATCCATGCACATTAGTGCCTGCCTGGCTGGTAAGGTAATGTATGATTCACTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAACAGTCTTGTGCTGTATTCTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTAGTAAGCAAGATAACCTTTTATTCAATTCA  
AGAATGGAATTTTTGTTCATGTCAGATTATTTGTATTTCTTTAACACTCTACATT  
TCCCTGTTTTAACTCATGCACATGTGCTTTGTACAGTTAAAAGTGTAAATAAAACTG  
ACATGTCAATGTGGCTAGTTTATTCTGTTGCATTATGTGATGGCCTGAAGTGTGGA  
CTTGCAAAAGGGAGAAGGAATTGCGAACATGTAAAATGTCACCAGACATTGTATTATT  
TTATCATGAAATCATGTTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTGAATGC  
ACAAAATGACTTAAACCATTCAATCATGTTCTTGCCTCAGCCAATTCAATTAAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT  
AVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPOEAEEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## **FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG  
CCGCAGGCTGCCCGCCGCTCCCTGCGCGCCGCCCTCCCGGACAGAAGATGTGCTCCAG  
GGTCCCTCTGCTGCTGCCGCTGCTCTGCTACTGGCCCTGGGCTGGGGTGCAGGGCTGCCCAT  
CCGGCTGCCAGTGCAGCCACAGACAGTCTTCTGCACTGCCCAGGGACCCACGGTGCC  
CGAGACGTGCCACCGACACGGTGGGCTGTACGTCTTGAGAACGGCATACCATGCTGACGC  
AGGCAGCTTGGCCCTGCCGGCTGCGACTCTGGACCTGTACAGAACCGATGCCAGCC  
TGCCCAGGGCTTCCAGCCACTGCCAACCTCAGCAACCTGGACCTGAGGCCAACAGGCTG  
CATGAAATACCAATGAGACCTCCGGCCTGCGCCCTCGACACGCTCGACGCCCTCTGGCAAGAA  
CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACGCCCTCTGGACCTCAAGCTGC  
AGGACAACGAGCTGCCGGCACTGCCCTGGCCTGCCCTGCCCTGCTGCTGCTGGACCTCAGC  
CACAAACAGCCTCTGGCCCTGGAGCCCGCATCCTGGACACTGCCAACGTGGAGGCCTGCGGCT  
GGCTGGTCTGGGGCTGCGCAGCTGGACGAGGGCTCTCAGCCGCTTGCACACCTCCACGACC  
TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCACACTGGCAGCCCTGAGTCCGAGGCCCTGGGGCTGACG  
CGCCTGCCGCTGCCGGCAACACCCGATGCCAGCTGCCGCCAGGACCTGCCGCCCTGGC  
TGCCCTGAGGAGCTGGATGTGAGCAACCTAACGCTGCCAGGCCCTGCCCTGGCACCTCTGGGCC  
TCTTCCCCCGCCTGCCGCTGCTGGCAGCTGCCGCAACCCCTCAACTGCGTGTGCCCTTGAGC  
TGGTTGGCCCTGGGTGCGCAGAGCCACGTACACTGGCAGCCCTGAGGAGACGCCGCTGCCA  
CTTCCCGCCAAGAACGCTGCCGGCTGCTCTGGAGCTTGACTACGCCGACTTGGCTGCCAG  
CCACCAACACCACAGCCACAGTGCCACCACAGGAGGCCCTGGTGCAGGCCACAGCCTTGCT  
TCTAGCTTGGCTCTACCTGGCTTAGCCCCACAGGCCGGCACTGAGGCCCCAGGCCGCCCC  
CACTGCCCAACCGACTGTAGGGCTGTCCTGGAGCCAGGACTGCCACCGTCCACCTGCCCTCA  
ATGGGGCACATGCCACCTGGGACACGGCACCACTGGCGTGTGCTTGCTGCCAGGCTTCAAG  
GCCCTGACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGGCCCTACACCAGTCAGCCAG  
GCCACCAACGGTCCCTGACCCCTGGGCATCGAGCCGGTGAAGGCCACCTCCCTGCGCTGGGGCTGC  
AGCGCTACCTCCAGGGAGCTCCGTGCACTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG  
GCCCTGATAAGCGCTGGTACGCTGCACTGCCCTGCCCTGCCCTGAGTACACGGTACCCA  
GCTGCCCAACGCCACTTACTCCGTCTGTGTCATGCCCTGGGCCCGGGCTGCCGAGG  
GCGAGGAGGCCCTGCCGGAGGCCATACACCCCAAGCCGCTCACTCCAACCCAGGCCAGTCACC  
CAGGCCCGAGGGCAACCTGCCCTCTCATGCCGCCCTGGCCGCGGTGCTCTGGCCG  
GCTGGCTGCCGAGGCCACTGTGTCAGGAGCCTGGGCCAGGAGCTGCCAGGCCAGGCC  
ACAAAGGGCAGGTGGGCCAGGGCTGGGCCCTGGAAACTGGAGGGAGTGAAGGCTCCCTGGAG  
CCAGGCCGAAGGCCACAGAGGGCGGTGGAGAGGCCCTGCCAGGGCTGAGTGTGAGGTGCC  
ACTCATGGCTTCCCAGGGCTGGCTCCAGTCACCCCTCCACGCAAAGGCCCTACATCTAAGCCA  
GAGAGAGACAGGGCAGTGGGCCGGCTCTCAGGCCAGTGAAGATGCCAGGCCAGGCCCTGGCC  
ACACCAACGTAAGTTCTCAGTCCCAACTCAGGAGATGTGTCAGACAGGGCTGTGACCAACAGCT  
GGGCCCTGTTCCCTGGAACCTCGGTCTCCATCTGAGATGCTGTCAGGAGCAGCTGACGAGCC  
CTAACGCTCCCAAGAACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCAACGTGCAAGTC  
CCTGGGCACGGCGGGCCCTGCCATGTGTCAGGCAACGCTGCCCTGGCCCTGCTGGCTCTCCAC  
TCCAGGGGACCCCTGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC  
GGCTGTGTGACTCTAGTCTGGCCCCAGGAAGCGAAGGAACAAAAGAAAAGAAACTGGAAAGGATGC  
TTTAGGAACATGTTTGTCTTTTAAATATATATTATAAGAGATCCTTCCCATTTATTCT  
GGGAAGATGTTTCAACACTCAGAGACAAGGACTTGGTTTGTAAAGACAACGATGATATGAA  
GCCCTTTGTAAGAAAAATAAAAGATGAAGTGTGAAA

## **FIGURE 16**

MCSRVPLLLPLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRPRLLLLDLSHNSLLALEPGILDGTANVE  
ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNLSQLALPGDLSGLFPRRLLLAAARNPFNCVCPLSWFGPWVRESHVTLASPEE  
TRCHFPPKNAGRLLLELDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHACLCPEGFTGLYCESQMGQGTRPSPTP  
VTPRPPRSLTGLIEPVSPSLRVGLQRYLQGSSVQLRSRLTYRNLSGPDKRLVTLRLPASIAEY  
TVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAYCVRGRAMAQQDKGQVPGAGPLELEGVKVPLEPGPKATEGGEALPSGSE  
CEVPLMGFPGPGLQSPHLAKPYI

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 579-599

**EGF-like domain cysteine pattern signature.**

amino acids 430-442

**Leucine zipper pattern.**

amino acids 197-219, 269-291

**N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

**Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

**N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646

## **FIGURE 17**

GCAGCGCGAGGCGCGGTGGCTGAGTCGTGGCAGAGGCGAAGGCGACAGCTCATGCG  
GGTCCGGATAGGGCTGACGCTGCTGCTGTGCGGTGCTGAGCTTGGCCTCGGCGTCCTCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTAGATTCCAAGACTACTTGACATCAGATGAGTCAGTA  
AAGGACCACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTCTTGATTCAAAGAAATCTGA  
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAG  
AAGATATCAGCTTCTAGAGTCCTCAAATCCAGAAAACAAGGACTATGAAGAGGCCAAAGAAAGTA  
CGGAAACCAGCTTGACCGCCATTGAAGGCACAGCACATGGGAGCCCTGCCACTCCCTTCT  
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAAGATGGCAGACTGTGGTGT  
CTACAACTATGACTACAAAGCAGATGAAAAGTGGGCTTTGTGAAACTGAAGAAGAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGAATGAAAATCTTAATGGAAG  
CAATAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTCAATGCTCTTATTGGTGATTACTGCCACAGAATATCCAG  
GCAGCGAGAGAGATTTGAGAAGCTGACTGAGGAAGGCCTCCCAAGGGACAGACTGCTCTGG  
CTTCTGTATGCCTCTGGACTTGGTGTAAATTCAAGTCAGGCAAAGGCTTTGTATATTACAT  
TTGGAGCTTGGGGCAATCTAAAGCCCACATGGTTTGTAAAGTAGACTTTAGTGGAAAGCT  
AATAATATTAACATCAGAAGAATTGTGGTTATAGCGGCCACAACCTTTCAGCTTCAATGATC  
CAGATTGCTGTATTAAGACCAAATATTCAAGTGAACCTCCTCAAATTCTGTAAATGGATAT  
AACACATGGAATCTACATGTAATGAAAGTGGTGGAGTCCACAATTTCCTTAAATGATTAG  
TTTGGCTGATTGCCCTAAAAGAGAGATCTGATAAAATGGCTCTTTAAATTCTCTGAGTTG  
GAATTGTCAAGATCATTTCATTTAGATTATCATAATTAAATTTCTTGTAAATGGATAT  
AAATTGTAAATGGTGGCTATAGAAAACAACATGAAATATTACAAATTGCAACAATGC  
CCTAAGAATTGTTAAAATTCACTGGAGTTATTGTGCAAGATGACTCCAGAGAGCTCTACTTCTG  
TTTTTACTTTCATGATTGGCTGTCTCCATTATTCTGGTCAATTATTGCTAGTGACACTGT  
GCCTGCTTCCAGTAGTCTCATTTCCATTGGTCAATTGTACTTTCTTGTAAATTGG  
AAGATTAACTCATTAAATAAAATTATGCTAAGATTAAGATTAAGATTAAGATTAAGATTAAG  
AAA

## **FIGURE 18**

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDESVKDHTTAGRVVAGQIFLDSEEESEL  
ESSIQEEEDSLKSQEGERVTEDISFLESPNPNENKDYEPPKKVRKPALTAIEGTAHGEPCCHFPFLFLDK  
EYDECTS DGDREDGRLWCATTYDYKADEKWGFCETEEEAKRRQMQEAEEMMYQTGMKILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFFGALGGNLIAHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## **FIGURE 19**

AATTCAAGATTTAACGCCATTCTGCAGTGGAAATTCACTGAACTAGCAAGAGGACACCATTCTT  
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTTTGGGTGCTAGG  
CCTCCTAATCCTCTGTGGTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGCTTGGAAACTTGGCAGCCAGAAACTTTGAT  
AAAAAGGGATTCATGTAATCGCTGCCTGCTGACTGAATCAGGATCAACAGCTTAAAGGCAGA  
AACCTCAGAGAGACTCGTACTGTGCTTGGATGTGACCGACCCAGAGAATGTCAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTGGGGAGAAAGGTCTCTGGGTCTGATCAATAATGCTGGTGT  
CCCAGCCTGGCTGGCTCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGA  
CCTGTTGGACTCATCAGTGTGACACTAAATATGCTCCTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAATGTCTCCAGTGTGAGGTCGCCTGCAATGTTGGAGGGGCTATACTCCATCCAAA  
TATGCAGTGGAAGGTTCAATGACAGCTTAAGACGGGACATGAAAGCTTGGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAACAAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC  
TCGCCATTGGAGCAGCTGTCTCCAGACATCAAACAAACATGGAGAAGGTTACATTGAAAAAA  
AGTCTAGACAAACTGAAAGGCAATAATCCTATGTGAACATGGACCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCAACAGTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAA  
TTTCTGGATAACCTGTTCACATGCCAGCAGCTTGAAGACTTTTATTGTTGAACAGAAA  
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCAAAATGCTCCTCCAGGCTATGA  
AATTGGCCGATTCAAGAACACATCTCCTTCAACCCATTCTTATCTGCTCCACCTGGACT  
CATTTAGATCGTCTTGGATTGCAAAAAGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT  
CCCTGCTCAAGTTCTTGAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCT  
GTATTTAGGCTTGCCTGCTTGGTGTGATGTAAGGAAATTGAAAGACTTGCCATTCAAAATGA  
TCTTACCGTGGCCTGCCCATGCTTATGGCCCCAGCATTACAGTAACTTGTGAATGTTAAGT  
ATCATCTCTTATCTAAATTAAGATAAGTCAACCCAAAAAAAAAAAA  
AAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGGLISVTLNMLPLVKKAQGRVINSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCIEPGLFKTNLADPVKVIKEKKLAIWEQLSPDIKQOYGEFYIEKSLDKLGNKSYVNMD  
LSPVVECMDHALTSLFPKTHYAGKDAKIFWIPLSHMPAALQDFLLLKQKAE LANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## **FIGURE 21**

CTGAGGCCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCGGGCTTGTGCTCGGCG  
CACTCGTTTCCAGCACCTAACACCGACTCGGACACCGAAGGTTTCTTCTGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTATACAATTGA  
CATTCAAGAAATATATTCCATGCTATCAGCTTTAGCTTATAATTCTTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTCAAGATCAGATCATGACGTTAGAGAGAGGCTGCTCACAAAACTTGCAGGAGCATT  
TTCAAAACCAAGACCTTGTCTGCTATTAAACACCAAGTATAAAACAGAAAGCTGCTACTC  
ATCGACTGGAACATCCTTATATAAACCTCAAAAGGACTTTACAGGGTACCTTAGTGGTT  
GCCAATCTGGCATGTCGAACAACGGTTATAAAACTGTATCAGGTTCTGTATGTCCACTGG  
TTTAGCCGAGCAGTACAAACACAGCTCAAATTTGAAGAAGATGGATCCTAAAGGAGG  
TACATAAGATAAAATGAAATGTATGCTTATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAACAGATTAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTCAAGGAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGA  
ACATTTTCTTGTCAAGGCATTACGGACCTTTTCAAATTCTGAATTCTTCAATTGTGTT  
ATGTCTTAAAAAATAGACATGTTCTAAAGTAGCTGTAACTACAACCACATCTCGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAACGATCCAAAAT  
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTGGTAATTACACGGTCTC  
CTACATTTGATCCCTTAAACCTTACAAGGAGATTTTATTGGCTGATGGTAAAGCCAAAC  
ATTCTATTGTTTACTATGTGAGCTACTTGCAGTAAGTICATTGTTTACTATGTTCAAC  
TGTTGAGTAATACACAGATAACTCTTAGTGCATTACTTCACAAAGTACTTTTCAAACATCA  
GATGCTTTATTCCAAACCTTTTCACTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG  
ACACATTCTTAAAGATAACTGGAAAAGTGAGACAGGACAGTGGCTCACACCTGTAATCCCAGCACT  
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGCAACGTATT  
GAGACCAGTCTATTAAAAAATGGAAAAGCAAGAATAGCCTTATTTCAAAATATGGAAA  
GAAATTATATGAAAATTATCTGAGTCATTAAAATTCTCCTTAAGTGATAACTTTTAAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAATTGCAAAACATCATCT  
AAAATTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI  
PCYQLFSFYNSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAV  
QTHSSKFFEDGSLKEVHKINEMYASLQEELKSICKVEDSEQAVDKLVKDVNLKREIEKRRGA  
QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVKSSCNYNHLDVVDNLTL  
MVEHTDIPEASPARTPQIIKHKALDDLDRQFKRSRLLDTQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

## **FIGURE 23**

GGCACAGCCGCGCGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGACGAGCGGACCAGCCAGGGCAGCCCAA  
GCAGCGCGCAGCGAACCCCCGCGCCGCCACACCCCTCGCGGTCCCCGCGGCCCTGCCACCCCTCCCTCCCTCCCC  
GCGTCCCCGCGCTCGCGGCCAGTCAGCTTGCGGGTTCGCTGCCCGCGAAACCCCGAGGTACCCAGCCGCGCTCT  
GCTTCCCTGGCCGCGGCCGCGCTCCACGCCCTCCTCTCCCGCTGCCCGCGCTGGCACCGGGGACCGTTGCCCTGA  
CGCGAGGCCAGCTCACTTTGCCCGCGCTCTCTCCCGCTGCCCTCTCCACCAACTCCAACCTCCCTCTCCCC  
TCCAGCTCCACTCGTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCCGCTTCCCGTCCGGTCCCAA  
GGTGGGAACCGCTCCGCCCGGCCGACCATGGCGACGGTTCGCGCTTGCCCGCGCTCTGCCACCCGGCAGTGC  
AGCGCCGCGCTGCCGTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCAGCTTACGTGTCCAAAGGCTTC  
AACAGAACGATGCCCGCTCCACGAGATCAACGGTGTCAATTGAAGATCTGCCCCAGGGTCTACCTGCTGCTCT  
CAAGAGATGGAGGAGAAGTACAGCTGCAAAGTAAAGATGATTCAAAGTGTGGTCAGCGAACAGTGAATCATTG  
CAAGCTGTCTTGCTTCACGTTACAAGAAGTTGATGAATTCTCAAAGAAACTACTTGAAAATGCAGAGAAATCCCTG  
AATGATATGTTGTGAAGACATATGCCATTATACATGCAAATTCTGAGCTATTAAAGATCTCTCGTAGAGTTG  
AACGTTACTACGTGGTGGAAATGTGAACCTGGAAAGAAATGCTAAATGACTCTGGGCTGCCCTGGAGCGGATG  
TTCCGCTGGTGAACCTCCAGTACCACTTACAGATGAGTATCTGGAATGTTGAGCAAGTATACGGAGCAGCTGAAG  
CCCTCGAGATGTCCTCGAAATTGAAGCTCCAGGTTACTCGTGTGTTGTACCGAGCCGTACTTCGCTCAAGGC  
TAGCGGGTGCAGGAGATGTCGTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG  
ATGATCTACTGCTCCACTGCCGGGTCTCGTGACTGTGAAGCCATGTTACAACATACTGCTCAAACATCATGAGAGGC  
TGTTGGCCAACCAAGGGATCTGATTTGAATGAAACAATTCTAGATGCTATGCTGATGGTGGCAGAGAGGCTA  
GAGGGTCTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTCTGATGCTATTATGAACATCGAGGAT  
AATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTCTCGT  
TCCATCTCTGAAAGTGCCTCGACTGCTCGCTCAGACCACATACCCAGGAACGCCAACACAGCAGCTGCCACT  
AGTTGGACCGACTGGTACTGATGTCAGGAGAAACTGAAACAGGCAAGAAATTCTGGCCTCCCGAGCAAC  
GTTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGAAAGGCAAAGCAGGTAC  
CTGTTGCAAGTGGATTAGCAACCAGGGCAACACCCAGGGTCCAGGTTGACACCAGCAAACAGAC  
ATACTGATCTCGTCAAATCATGGCTCTCGAGTGTGACCAAGATGAAGATGCTACAAATGGAACGACGTG  
GACTTCTTGATATCAGTGTGAAAGTAGTGGAGAAGGAAGTGGAGTGGCTGTGAGTATCAGCAGTCCCTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGAGTGGCTGCAATGAGAAAGCCGACAGTGTGGTCCGTCTGGGCA  
CAGGCCTACCTCTCACTGCTCTGCATCTGTTCTGGTTATGCAGAGAGACTGGAGATAATTCTCAAACACTGAG  
AAAAAGTGTCTCAAAAGTTAAAGGCACCGTTATCACTTTCTACCATCTAGTGAATTGCTTTAAATGAA  
TGGACAACAATGTACAGTTTACTATGTGGCACTGGTTAAGAAGTGTGACTTGTGTTCTCATTCAGTTGG  
AGGAAAGGGACTGTGATTGAGTTGGCTCTGCTCCCCAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTTGTGCATTGTGATTGAGTTGGCTCTGCTGGGTTATGTTTGTGTTCTCATTCAGTTGTGGGTT  
TTTTTCTCAACTGTGATCTCGCTTGTGTTTACAAGCAAACAGGGTCCCTTGTGGCACGTAACATGTACGTATT  
TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTATTATCATGTTATCTTAAAGAAAAAGCCAAAAGC

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAELKS KSCSEVRR LYVSKG F N KND APLHEINGDHLKICPQGST  
CCSQEME EK YSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKS LNDMFVKT YGH  
LYMQNSELFKDLFVELKRYYVVG NVNLEEMLNDFWARLLERMFR LVNSQYHFTDEYLECVSKY TE  
QLKPF GDV PRKLKLQVTRAFVAARTFAQGLAVAGDV VSKVSVNPTAQC THALLKMIYCSHCRGL  
VTVKPCNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKV FQGC GPPKPLPAGRISRSI SEAFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSLPSNVCN DERMAAGNGNE DDCWNGKGSRYLFATGNGLANQGNP E VQV DTS  
KPDILILRQIMALRVM TSKMKNAYNGNDVFFF DISDESS GEGSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGV RPGAQAYLLTVFCILFLVMQREW R

**Important features:**

**Signal peptide:**

amino acids 1-22

**ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

**N-glycosylation site.**

amino acids 514-518

**Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

**N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

**Glycans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## **FIGURE 25**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTCCATTATATTCTTCAGCAACT  
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTCCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGCTCTAGCAGCCTGAATCCAGGGTCGCCAGAGGCCACAGGGACCGAGGC  
CAGGCTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTCCTGAG  
AGCCCCGAGAAGAAAATTATGACAGTGTCTGGGCTGCCAAGAAGCAGTGCCCCCGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAAGGCACCACAGAAAGCCAACAAGCATTCCAGA  
GCCTGCCAGCAATTCTCAAACATGTCAGCTAAGAAGCTTGCTGCCCTTGTAGGAGCTCTG  
AGCGCCCACTCTTCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC  
TTCTTCTCCCACCTCACTCTCCACTGTACCCACCCCTAAATCATCCAGTGCTCTCAAAAGCA  
TGTTTTCAAGATCATTGTTGCTCTCTAGTGTCTCTCTCGTCAGTCTTAGCCT  
GTGCCCTCCCTAACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCC  
AGCTAGTGTCAATTAAACCTAAATGCAATCAGGAAAGTAGCAAACAGAAAGTCAATAAATATTTT  
AAATGTCAAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISSLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKQCPDCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## **FIGURE 27**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAGCCAGTGCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTCTGCTTCTTACCCCTGCC  
CCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCCGTGCAAAAGCTACTTCCCCTACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTTCAGCCAG  
ATAAAGGGCTTACAGGAGCCTCCGGAAAGTGGCCCTACTGGAGCTGGCTGCCAACCGGAGC  
CAACTTCAGTTCTACCCACCAGGCTGCAGGGCACCTGCCTAGACCCAAATCCCCACTTGAGA  
AGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCAATATGAGCGGTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGCTGCACCTGGTGTG  
CTCTGTGCAGAGCCAAGGAAGGTCCCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTG  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGAAAGCTGGCTCATGTGGCAGCAAGTTTC  
GAGCCCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAAGAGAGACCTGGAAGGATCTGA  
GAACGCCAGTTCTCGAAATCCAATGGAACGACAGCCCCCTCCCTGAAGTGGCTACCTGTT  
GGCCCCACATCATGGGAAAGGCTGTCAAACATCTTCCCAAGCTCCAAGGCACTCATTGCTCC  
TTCCCCAGCCTCCAATTAGAACAGCCACCCACCAGCTATCTATCTTCACTGAGAGGGACCTA  
GCAGAAATGAGAGAACATTGATGTACCCACTAGTCCCTCTCCCCAACCTCTGCCAGGGC  
AATCTCTAACTCAATCCGCCCTCGACAGTGAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCCTGTTGATCTCAACTGCAAGTTCTGGACTAGTCTCCCAACGTTGCTC  
CCAATGTTGTCCTTCCCTCGTTCCATGGTAAAGCTCTCTCGCTTCTCTGAGGCTACAC  
CCATGCGTCTCTAGGAACCTGGTCAAAAAGTCATGGTGCCTGCATCCCTGCCAACGCCCCCTGAC  
CCTCTCTCCCCACTACCACCTCTCCCTGAGCTGGGGGCCACCAGGGAGAAATCAGAGATGCTGGG  
ATGCCAGAGCAAGACTCAAAGAGGGCAGAGGTTTGTCTCAAATATTTTTAATAAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPPLLQLLVLLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQIKGL  
TGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDVVVCTLVLCSVQSPRKVLQEVRRVLRPGGVLFVWEHVAEPYGSWAFMWQQVFEPTW  
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFPSKALICSFPSL  
QLEQATHQPIYLPRLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

## **FIGURE 29**

CAATGTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTAAAGGCTCATGCTGGAGTGGGGACTGGTCGGTCCCCAGAAAGTCTCTCTG  
CCACTGACGCCCCATCAGGGATTGGGCCTCTTCCCCCTTCCTTGTGTCTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGTGGGGATGGCTA  
AGAAAGCTGGGAGATAGGGAACAGAACAGAGGGTAGTGGGTGGCTAGGGGGCTGCCTTATTTAAA  
GTGGTTTTATGATTCTTATACTAATTTACAAAGATATTAAGGCCCTGTTCATTAAGAAATT  
GTTCCCTTCCCTGTGTTCAATGTTGTAAGATTGTTCTGTGTAATATGTCTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## **FIGURE 31**

GTTCAGATTCCCTCAACTATAACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT  
CCTCCAAGCAAGTCATTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
ATTTGCATCTGTTGATAAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGAATCATGTCGG  
GAAGAGATAACAATCCTGGCCTGTGTATCCTCGCATTAGCCTGTCTTGGCCATGATGTTACC  
TTCAGATTCATCACCAACCCCTGGTTCACATTCATTGGTTATTTGGGATTGTTGTT  
TGTCTGCGGTGTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
CAGAAAGGAAAATATGAAGTGGCTGGGTTGCTATCGTATCCACAGGCATCACGGCAGTG  
CTGCTCGTCTGATTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTCCAAATCAC  
AAATAAAGCCATCAGCAGTGCTCCCTCCTGCTGTTCCAGCCACTGTGGACATTGCCATCCTCA  
TTTCTCTGGGTCTCTGGGTGGCTGTGCTGAGCCTGGAAACTGCAGGAGCTGCCAGGTT  
ATGGAAGGCGGCCAAGTGGAAATATAAGCCCTTCGGCATTGGTACATGTGGTGTACCATTT  
AATTGGCCTCATCTGGACTAGTGAATTCATCCTGCGTGCCAGCAAATGACTATAGCTGGGCAG  
TGGTTACTGTTATTCACAGAACTAAAGTAACTGCTGCTGAGCCTGGTACATGGTGTACCATTT  
TCCATTCTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCACTGGTACATGGTGTACCATC  
GATTGGAGAATCATTGTACATGCAAAACGACTGAAAGAACAGCAGCATGGTGCATTGT  
CCAGGTACCTGTCGATGCTGACTGCTGTTCTGGTGTCTGACAAATACCTGCTCCATCTC  
AACCGAGATGCATATACTACAACGTATTAACTGGACAGATTCTGTACATCAGCAAAGATGC  
ATTCAAATCTTGTCCAAGAACTCAAGTCACTTACATCTATTAACTGCTTGGAGACTTACAA  
TTTTCTAGGAAAGGTGTTAGTGGTGTGTTCACTGTTGGAGACTCATGGCTTTAACTAC  
AATCGGGCATTCCAGGTGTGGCAGTCCCTCTGTTATGGTAGCTTTGCCTACTTAGTAGC  
CCATAGTTTTATCTGTGTTGAAACTGTGCTGGATGCACCTTCTGTTGCTGTTGATC  
TGGAAACAAATGATGGATCGTCAGAAAAGCCACTTTATGGATCAAGAATTCTGAGTTCGTA  
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA  
GGGAACAGAACTCCAGGCCATTGTGAGAATAGATACCCATTAGGTATCTGTACCTGGAAAACATT  
TCCCTCTAAGAGCCATTACAGAAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATT  
TTAAAGACCTAATAAACCTATTCTCCTCAAA

## **FIGURE 32**

MSGRTDTILGLCILALALSLAMMFTFRFITTLLVHIFISLVLGILFVCGVLWWLYYDYNLDSIE  
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISAPFLFQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA  
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIVMMQNALKEQQHG  
ALSRYLFRCYCFCWCLDKYLLHLNQNAYTTAINGTDFCTSAKDAFKILSKNSHFTSINCFGD  
FIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

**Important features:**

**Signal peptide:**

amino acids 1-20

**Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

**N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

**N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

### **FIGURE 33**

## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR  
ESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA  
TPPTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNRPRADEPGIQRQDPGAAFKQP  
VGADVSLGLVPKEELSTSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNVVVVVMDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTQPLVKRVCDDRLACSKTCLNSADIGFVIDGSSSGTGNFRVTLQFVTN  
LTKEFEISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGWSSGGTSTGAAINFALEQL  
FKKSCKPNKRKLMILITDGRSYDDVRIPAMAHLKGVITYAIGVAWAQEELEVIATHPARDHSFF  
VDEFDNLHQYVVPRIIQNICTEFNSQPRN

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 181-200

**N-glycosylation sites.**

amino acids 390-394, 520-524

**N-myristylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

**Amidation site.**

amino acids 304-308

## **FIGURE 35**

CCGAGCACAGGAGATTGCCTGCCTTAGGAGGTGGCTGCCTGTGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGCTTTCTGTTCAAGAGTAGTTACAACAGATCTGAGTGTTTAATTAAGCATGGAAT  
ACAGAAAACAACAAAAACTTAAGCTTAATTCATCTGGAATTCCACAGTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTTGGCTCTCCCGCTGGCTGCTCTACACGTGGTGCTCTCCGACTACTCACCCCGAGTGTA  
AAGAACCTCGGCTCGCGTCTGAGCTGCTGTGGAGGCCCTCGGCTCTGGACTGTCTCCGAGTA  
GGATGTCACTGAGATCCCTAAATGGAGCCTCTGCTGTCACTCCTGAGTTCTTGATGTGGTAC  
CTCAGCCTCCCCACTACAATGTGATAGAACCGGTAACTGGATGACTTCTATGAGTATGAGCCGATT  
CAGACAAGACTTCACTCACACTCGAGAGCATTCAAACAGCTCTCATCAAAATCCATTCTGGTCATT  
TGGTGACCTCCACCCTCAGATGTGAAAGCCAGGCCATTAGAGTTACTGGGGTGAAGAAAAGTCT  
TGGTGGGGATATGAGGTTCTTACATTTCTTATTAGGCCAAGAGGCTGAAAGGAAGACAAAATGTTGGC  
ATTGTCCTTAGAGGATGAACACCTCTTATGGTACATAATCCGACAAGATTTTAGACACATATAATA  
ACCTGACCTTGAACACCATTATGGCATTCAAGGTGGTAACACTGAGTTTGCCCCAATGCCAAGTACGTAATG  
AAGACAGACACTGATGTTCATCAAACTGGCAATTAGTGAAGTATCTTAAACCTAAACCACTCAGA  
GAAGTTTACAGGTATCCTCTAATTGATAATTATTCTATAGAGGATTACCAAAAACCCATATT  
CTTACCAGGAGTATCCTTCAAGGTGGTCCACTGCAGTGGGTGGTTATATAATGTCAGAGAT  
TTGGTGCCAAGGATCTATGAAATGATGGTCACGTAAACCCATCAAGTTGAAGATGTTATGTCGGGAT  
CTGTTGAATTATAAAAGTGAACATTCAATTCCAGAACAGACACAAATCTTCTTCTATAGAATCC  
ATTGGATGTCTGTCAACTGAGACGTGTATTGCAGCCCATTGGTTCTTCAAGGAGATCATCACTTT  
TGGCAGGTATGCTAAGGAACACCAATGCCATTTAACTCACATTCTACAAAAGCCTAGAAGGACAG  
GATACCTGTGAAAGTGTAAATAAGTAGGTAACGTGGAAACTGGAGACTGGAGGGTTACACTGTGATTAGTCAGG  
CCCTCAAAGATGATATGTGGAGGAATTAAATATAAGGAATTGGAGGTTTGCTAAAGAAATTAGG  
ACCAAACAATTGGACATGTCAATTGTAGACTAGAAATTCTAAAGGTGTTACTGAGTTATAAGCTCA  
CTAGGCTGTAAAACAAAACATGTAGAGTTTATTTATTGAACAAATGTGACTTGAAGGTTTGTTGTA  
TATCTTATGTGGATTACCAATTAAAAATATGTAGTTCTGTGTCAAAAACTCTTCACTGAAGTTATA  
CTGAACAAAATTACCTGTGTTGGTCATTATAAGTACTTCAAGATGTTGCAGTATTCACAGTTATT  
ATTATTTAAAATTACTTCACATTGTGTTTAAATGTTTGACGATTCAACAAAGATAAAAAGGAGATAG  
TGAATCATTCTTACATGCAAACATTCCAGTTACTTAACGTGATCAGTTATTATTGATAACATCACTCCA  
TTAATGAAAGTCATAGGTCAATTGCATATCAGTAATCTTGGACTTTGTTAAATTTACTGTGGT  
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHF  
TLREHSNCNSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFFLLGQEAEKEDKMLA  
LSLEDEHLLYGDIIRQDFLDTYNNLTLKТИMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV  
KPIKFEDVYVGICLNLLKVNIIHIEDTNLFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

**Important features:**

**Type II transmembrane domain:**

amino acids 20-39

**N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

**Glycosaminoglycan attachment site.**

amino acids 239-243

**Ly-6 / u-PAR domain proteins.**

amino acids 23-37

**N-myristoylation site.**

amino acids 271-277

### **FIGURE 37**

## **FIGURE 38**

MELGCWTQLGLTFLOLLLSSSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQII  
KRCVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC  
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNSYVLSNE  
KRTCQONGEWSGKQPIKACREPCKISDLVRRRVLPMQVSRETPLHQLYSAAFSKQKLQSAPTK  
KPALPGDLPGMGYQHLHTQLOQECISPFFYRRLGSSRTCLRTGKWSGRAPSCIPICGKIENITAP  
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDDREKTIQSLQISAIILHPNYDPILLDAIDIAILKLLDKARISTRVQPICLAASR  
DLSTSFAQESHITVAGWNVLADVRSPGFKNDSLRSGVSVVDSLLCEEQHEDHGIIPVSVTDNMFCA  
SWEPTAPS DICTAETGGIAAVSFPGRASPEPRWHLMGLVWSYDKTCSHRLSTAFTKVLPEFKDWI  
ERNMK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**EGF-like domain cysteine pattern signature.**

amino acids 260-272

**N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

**N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

**Amidation site.**

amino acids 56-60

**Serine proteases, trypsin family.**

amino acids 489-506

**CUB domain proteins profile.**

amino acids 150-167

## **FIGURE 39**

GGTTCCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTACGGGCCGTGATTTATTAACGTGGCTTAATC  
TGAAGGTTCTCAGTCAAATTCTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTGCTTAAAGGAGCTTGGCTGG  
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTGC  
TGGTCTTGCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGCAACCTGCACCTCCTGTATTCAAGAACTCTGTA  
AAGGTGCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCCCTACAAAGATGGCTGTCCAGACGCCGTGCGAGCC  
TCACAGCCACGGCTCCCTCCCCAGAGGTTCTGCAGCTGCCACCCTCCTTAATGACAGACGAGCCTGGCTAGACA  
ACCCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGGCCATCAGCCAGTGGACTCTGCCGGAGCAACCGAAGCTA  
GGGCACGCCCTTGAGAGATCCACTATTAGAACAGATCAATTAAAAAAATAATCGAGCTTGAGTGTCTCGAA  
GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCACCAGGGCAGGGAAATTCTGAAAACACCACTGCCCTGAAG  
TCTTCCAAAGGTGTACCACTGATTCCAGATGGTGAATTACAGCATCAAGATCAATGAGTAGATCCCAGTGAAA  
GCCTCTCTATTAGGCTGGTGGAGGTAGCGAAACCCCCACTGGTCCATATCATTATCCAACACATTATCGTATGGGG  
TGATCGCCAGAGACGGCGCTACTGCCAGGAGACATCATTCTAAAGGTCACAGGGATGGACATCAGCAATGTCCTC  
ACAACATACGCTGTGCGCTCCTGCCGGCAGCCCTGCCAGGTGCTGGCTGACTGTGATGCGTGAACAGAAGTCCGCA  
GCAGGAAACAATGGACAGCCCCGGATGCCTACAGACCCCGAGATGACAGCTTCATGTGATTCTCAACAAAAGTAGCC  
CCGAGGAGCAGTTGGAAATAAACTGGTGGCAAGGTGGATGAGCCTGGGTTTTCATCTCAATGCTGGATGGCG  
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCA  
GCCCAAGAAAGTGGCGCTCATCTGATTCAAGGCCAGTGAAAGACGTGTTCACCTCGTGTCCCGCCAGGTTGGCAGC  
GGAGCCCTGACATCTTCAGGAAGCCGGCTGGAACAGCAATGCCAGCTGGTCCCCAGGGCAGGGAGAGGAGCAACA  
CTCCCAAGCCCCCATCTACAATTACTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCGGTGAATCTCTCG  
GCATGACCGTGCAGGGGAGCATCACATAGAGAATGGGATTGCTATCTATGTCATCAGTGTGAGCCGGAGGAG  
TCATAAGCAGAGATGGAGAATAAAACAGGTGACATTGTTGAATGTTGAATGGGATGGGTCGAACGTACAGAGGTGAGC  
GGAGTGAGGAGCTGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTGGAAAGTCAAAGAGTATGAGC  
CCCAGGAAGACTGCAGCAGGCCAGCAGCCCTGGACTCCAACCACAAACATGGCCCCACCCAGTGACTIONGTCCTCC  
GGGTGATGTGGCTGGATTACACCGTGTTGTATAACTGTAAGATATTGTTACGAAGAACACAGCTGGAGTC  
TGGGCTCTGCAATTGAGGAGTATTGAGAATACATGAAACAAACCTTTTCATCAATCATTGTTGAAGGAA  
CACAGCATAATGATGAGAATTAGATGTGGTATATTCTCTTGCTGTCATGGTAAAGTACATCAGGAATGA  
TACATGCTTGCTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTCTGGCTGGCACTT  
TTTTATAGAATCAATGATGGGTAGAGGAAACAGAAAAATCACAAATAGGCTAAGAAGTGAACACTATATTATC  
TTGTCAGTTTATATTAAAGAAAATACATTGAAAAATGTCAAGGAAAGTATGATCATCTAATGAAAGCCAGTT  
ACACCTCAGAAAATATGATTCAAATTTAAACTACTAGTTTTTCAGTGTGGAGGATTCTCATTACTCTAC  
AACATTGTTATATTCTATTCAATAAAAGCCCTAAACAACTAAATGATTGATTGTATACCCACTGAATT  
CAAGCTGATTAAATTAAATTGGTATATGCTGAAAGTCTGCCAGGGTACATTATGCCATTTTAATTTACAGCT  
AAAATTTTAAATGCATTGCTGAGAACGTTGCTTCATCAAACAAGAATAATTTTACAGTTAAA

## **FIGURE 40**

MKALLLLVLPWLSPTYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDGASLTATAPS  
PEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSRSFKKINR  
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV  
GGSETPLVHIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFI FNVLDDGVAYRHG  
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSRQRSPDIFQEAGWNSNGSWSPG  
PGERSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
IKTGDILLNVDGVELTEVRSEAVALLKRTSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP  
SDWSPSPWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLRLLKELKGRITLTIVSWPGTFL

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## **FIGURE 41**

ACCAAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTT  
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAACATGGGCTTCAACCTGACT  
TTCCACCTTCCTACAAATTCCGATTACTGTTGCTGACTTGTGCCTGACAGTGGTGGGTGGC  
CACCAAGTAACTACTTCGTGGGCCATTCAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTCC  
ATAAGACCCCTCATTTGGGAGGGAAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT  
GACAACGTGCTTCTGTGTCTCCTACCTCAGAGGCCAGAGCAAGCTCATTTCAAACCAAGATCTCAC  
TTTGGAAAGAGGTACAGGCAGAAAATCCAAAGTGTCCAGAGGCCGGTATGCCCTCAGGAATGTAAG  
CTTACAGAGGGTGCCTACCTCGTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGG  
TAAAAAGTTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTAAGGAAGAAAATTGGG  
ACTGCTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTACAAGTGTGAGGAG  
CATCCCAAGCATCTGGTGGTGGCAGGAACAGCACTGGGTACAGGTACAGTGGATATTGG  
GGGTGTACTGCCCTAACAGCAGAGAGCAGTTTCAAGGTGAATGGATTCTCTAACAACTACTGGGAT  
GGGGAGGCAGACGATGACCTCAGACTCAGGGTGAGCTCCAAAGAATGAAAATTCCCGCCCTG  
CCTGAAGTGGTAAATATAACATGGCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTTACACCAAGTGTACAGACTGGAGAACAGATGGTTGAGTAGTTGTTCTTAAAT  
TAGTATCTGTGGAACACAATCCTTATATATCAACATCACAGTGGATTCTGGTTGGTGCATGACCC  
TGGATCTTGGTGTGATGTTGGAAGAACTGATTCTTGTGCAATAATTGGCTAGAGACTTCAA  
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTCCTTGTATTCT  
TAGCAGAGCTCCTGGTGTGAGTAGACTAAAAACAGTTGTAACAAGACAGCTTCTAGTCATTGAT  
CATGAGGGTTAAATATTGTAATATGGATACTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTGAGGACTCTGGTGAAGGAGATTATTAAATTGAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCCAGAGTTGTTCTCGTCCAAGGTAGAA  
AGGTACGAAGATAACAATACTGTTATTCAATTCTGTACAATCATCTGTGAAGTGGTGGTGTCAAGGT  
GAGAAGGCCTCACAAAGAGGGAGAAAGGCCAGCAATCAGGACACAGTGAACATTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAGGCAGCAGTAGCTGAGCTGGTGCAGGTGCTGATAGC  
CTTCAGGGAGGACCTGCCAGGTATGCCTCCAGTGTGATGCCACCAGAGAAATACATTCTATTAGT  
TTTAAAGAGTTTGTAAAATGATTTGTACAAGTAGGATATGAATTAGCAGTTACAAGTTACAT  
ATTAACATAATAATATGTCTATCAAATACCTCTGTAGTAAATGTGAAAAGCAAA

## **FIGURE 42**

MGFNLTFHLSYKFRLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTILIGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDILTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHLMYLLEHLHPFLQRQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFIFHDV  
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVITALSREQFFKVNGFSNNYWGWGGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

### **FIGURE 43**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCAGATCTGGG  
CCGCTTGCCTCCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTCCCACAAACAG  
ACGGGACAACCTGCAGAGCTGCAACCCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCAT  
GTTCCAGAGGCAGAGGAGGCAGACACCCACTTCCCCATCTGCATTCTGCTGCGGCTGCTGTC  
ATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTGCCCCGTCCCCCTCCC  
TTCCTTATTATTCCCTGCTGCCAGAACATAGGTCTTGAATAAAATGGCTGGTTCTTTGTTT  
TCCAAA  
AAA

## **FIGURE 44**

MALSSQIWAACLLLLL~~LL~~ASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTHFPI  
CIFCCGCCHR~~S~~KCGMCCKT

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

**N-myristoylation site.**

amino acids 44-50

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

## **FIGURE 45**

GTGGCTTCATTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTCCCCAACATGCCTCACCC  
TCATCTATATCCTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCGTGAAGAGCTGGTCGGT  
TCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTCTATTGCTG  
GACCTTCAACACAACCCCTTGTCAACCATACAGCCAGAAGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAG  
AAGAATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCAGCAGCCCTCCACCCA  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCTAAAGTCACCATGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGCAAGCAGCCAATGAGTCCATAATGGTCCATCCTCCCCATCTC  
CTGGAGATGGGAGAAAGTGTATGACCTCATCTCGTGCAGGAACCTGTCAGCAGAAACT  
TCTCAAGCCCCATCCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG  
GTCCTCCTGTGTCTCTGTTGGTGCCTCCTGCTCAGTCTTTGACTGGCTATTCCTTG  
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGGTGGACATTGTCGGG  
AAACTCTAACATATGCCCTATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAAATCTAACAGAACATCCAGCAAATACGGTTACTCCACTGTGGAAATACCGAAAAAGAT  
GGAAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCTAACGTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLSKVKQVDSIVWTFTTPLVTIQP  
EGGTIIVTQNRNRERVDFPDGGYSLKLSKLNNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK  
PKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC  
VARNPVSRNFSSPILARKLCEGAADDPSSMVLLCLLVPPLLSLFVLGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## **FIGURE 47**

GGCTCGAGCGTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCAATGCGATACCTCTAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTCTCAAAACCCATCTCTGCTTGAGTGGGGTCCCAGGAATT  
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACTGGAATGTTCTTCATCATTTCAGTGTGATCACAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTAAAGGTCTCTCATGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTAATTTCATTGAAAAACATCAGTGACATTCCAGAATCCTCAA  
CTTGAGTGGTTTCAATGACTCTTGTGACCTCCTACTGGTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCACTTCGATTCTGAAGAAAACAAACATAGG  
CTTATCCACTCTCAGTATTTAGGTCTATTGCTTGGAAATTCTGGAGGTCTGTTGGCT  
CAGTCAGATAGTCATGGTTCCGGCTGTCTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG  
TGTAGTTAATGGAATAAAATGTAAGTATCAGTAGTTGAAAAA

## **FIGURE 48**

MTCCEGWTSCNGFSLVLLLGVVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCMILISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

**Important features:**

**Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

**N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

**N-myristylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

**TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## **FIGURE 49**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCCCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTCGAACTGTGA  
CATGGAGAGAGTGACCTGGCCCTCTCCTACTGGCAGGCCTGACTGCCCTGGAAGCCAATGACC  
CATTTGCCAATAAAGACGATCCCTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGCAGGGGCTCGGCCATTGCTGGGATCGCGCAGTCTGAGTGGCAAATGAAATACAAGAG  
CAGCCAGAACGACAGTCTGTACCTGAGAAGGCCATCCACTCATCACTCCAGGCTCGCCA  
CTACTTGCTGAGCACAGGACTGGCCTCCAGGGATGGCTGAAGCCTAACACTGCCACCAGCACC  
TCCTCCCTGGAGGCCTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCT  
TTCTGATCAGGAGGCTTATGAATTAAACTGCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLAIAGIAAVLSGKCKYKS  
SQKQHQHSPVPEKAIPPLITPGSATTC

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## **FIGURE 51**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGGAAGGAGGGACAGAGGGCACAGAGACGCAGAGCAAGGGCGCAAGG  
AGGAGACCCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAGATGAAGTCCAG  
GGGCCCCCTGGCCTGCCTCTGGCCCTCTGCCTGGCAGTGGGAGGCTGGCCCTGCAGAG  
CGGAGAGGAAGCACTGGACAAATATTGGGGAGGCCCTGGACATGGCCTGGAGACGCCCTGA  
GCGAAGGGGTGGGAAAGGCCATTGCAAAGAGGCCGGAGGGCAGCTGGCTCTAAAGTCAGTGAG  
GCCCTGGCCAAGGGACCAGAGAAGCAGTGGCACTGGAGTCAGGCAGGTTCCAGGCTTGGC  
AGCAGATGCTTGGCAACAGGTGGAAAGCAGCCATGCTCTGGAAACACTGGCAGCAGA  
TTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCAGATGCTGTCCGGCTCTGGCAGGG  
GTGCCTGGCCACAGTGGCTTGGAAACTCTGGAGGCCATGGCATTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCAAGGGCAATCCTGGAGGTCTGGGACTCCGTGGTCCACGGATAACCCG  
GAAACTCAGCAGGCAGCTTGAATGAATCCTCAGGGAGCTCCCTGGGCAAGGAGGCAATGGA  
GGGCCACCAAACATTGGGACCAACACTCAGGGAGCTGGCCAGCCTGGCTATGGTCAGTGAG  
AGCCAGCAACCAGAATGAAGGGTGCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGAGGCAGCGCTCACAGTCGGCAGCAGTGGCAGTGGCAGCAATGGTACAACAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAG  
TGGCGCAGCAGTGGTGGCAGCAGTGGCAACACTGGTGGCAGCAGGAGGTGACAGCGGAGT  
CCTCCTGGGATCAGCACCGCTCCTCTCCGGCAACCACGGTGGAGCGGGAGGAAATGGA  
CATAAACCCGGGTGTGAAAAGCCAGGGAAATGAAGCCGGAGCGGGGAATCTGGGATTCAAGGG  
CTTCAGAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTTGG  
GAGGCTCTGGAGACAATTATCGGGGCAAGGGTGAGCTGGGAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCATACTGTGAACCTGAGACGTCTGGGATGTTAACCTTGACACTTCTGGAA  
GAATTTAAATCCAAGCTGGTTCATCAACTGGGATGCCATAAACAGGACCAAGAGCTCTC  
GCATCCCGTGACCTCCAGACAAGGAGCCACAGATTGGATGGAGCCCCCACACTCCCTTAA  
AACACCAACCCCTCATCACTAAATCTCAGCCCTGGCCTTGAAATAACCTTAGCTGCCCAAAA  
AAA  
AAA

## **FIGURE 52**

MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVS  
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGP  
GHSGAWETSGGHGIFGSQGGLGGQGQNPQGLGTPWVHYPGNSAGSFGMNPQGAPWGQGGNGPPNF  
GTNTQGAVAQPGYGSVRASNQNEGCTNPPSGSGGGSSNSGGSGSQSGSSGSGNSGDNNNNGSSGGS  
SSGSSSSGSSGGSSGGSSGSSGSGSNGSGSGDGSSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNE  
ARGSGESGIQGFRGQGVSSNMREISKEGNRLGGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGM  
FNFDTFWKNFKSKLGFNWDAINKDQRSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## **FIGURE 53**

GGAGAAAGAGGTTGTGGGACAAGCTGCTCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG  
CTGGGCTCAGACCGGTGGCAATGTCCTGGCTACTCCTGCTGCTGGTGTGGCTCCTGGCT  
ACTCGCCCGCATCCTGGCTGGACCTATGCCCTCTATAACAACGCGCCGGCTCCAGTGTTC  
CACAGCCCCAAACCGAACGTTGGGTCACCTGGCCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGGGCTTACGGTATGGCTGGTCCC  
CATCCCCCTCATGCTTATGCCACCCGACACCCTGGCTATCACCAATGCCCTCAGCTGCCA  
TTGCACCCAAGGATAATCTCTCATCAGGTTCTGAAGCCCTGGCTGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGGCCACCGTCGGATGCTGACGCCCTGGCTTCCATTCAACATCC  
GAAGTCTATATAACGATCTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGTCGGACATGTTGAGCACATCAGCTCATGACCTGGACAGTCTA  
CAGAAATGCACTTCAGCTTGACAGCCATTGTCAGGAGAGGCCAGTGAATATATTGCCACCAT  
CTTGGAGCTCAGTGCCCTGTAGAGAAAAGAACGCAGCATATCCTCCAGCACATGGACTTCTGT  
ATTACCTCTCCATGACGGGGCGCTTCCACAGGGCCTGCCGCTGGTGCATGACTCACAGAC  
GCTGTCATCCGGAGCGCGTCGCACCCCTCCCCACTCAGGGTATTGATGATTTCAAAGACAA  
AGCCAAGTCCAAGACTTGGATTCATTGATGTCGCTTGAGCAAGGATGAAGATGGGAAGG  
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTCATGTTGGAGGCCATGACACCACG  
GCCAGTGGCCTCCTGGTCTGTACAACCTTGCAGGCCACCCAGAATACCAGGAGCGCTGCCG  
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCAGTCTAAAGAGATTGAATGGGACGACCTGCC  
AGCTGCCCTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTCATC  
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGCCGAGTCATCCCCAAAGGCATTACCTG  
CCTCATCGATATTATAGGGTCCATCACAACCCAACTGTGTCGGCCGAGTCATCCCCAAAGGCATTACCTG  
CCTTCCGTTTGACCCAGAGAACAGCAAGGGAGGTCAACCTCTGGCTTTATTCCCTTCTCCGCA  
GGGCCAGGAACTGCATGGCAGGCAGTCGCCATGGGGAGATGAAAGTGGCCTGGCGTTGAT  
GCTGCTGACTTCCGGTTCTGCCAGACCAACTGAGCCCGCAGGAAGCTGGAATTGATCATGC  
GCGCCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCAGACTTCTGAC  
CCATCCACCTGTTTTGCAAGATTGTCATGAATAAACGGTGCTGTC  
AAA

## **FIGURE 54**

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRLQCFPQPPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGEGLLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYILSHDGRRFHRAC  
RLVHDFTDAVIRERRTLPTQGIDDDFKDKAKSKTLDFIDVLLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWVLYNLRHPEYQERCRCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPPEVYDPFRFPENSKGGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

**Important features:**

**Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

## **FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTGA  
GCCTACTCGTTGATTGCAACTATCATGGTGTGTTGCACTTACCCCTGTGTTGCCT  
TTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTGCAGTCTTGGCATTGACGTGG  
TACAGCCTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCCGTGTCTTGC  
ATAATTCATGGCCAGTTTATGAAGCTTGAAGGCACTATGGACAGAAGCTGGTGGACAGTTT  
GTAACATCTCGAACACCTCTGTCTTACAGACATGTGCCCTTATCTTGCAGCAATGTGTTGCTT  
GTGATTGAAACATTGAGGGTTACTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAAATCTCCTCATGTACCTGTTCCCTC  
TCTGGATGTTGTCCCACTGAATTCCCATGAATAACAAACCTATTCAACAGCAACAGCAAAAAAAAAAAA  
AA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWHNKGLALIFCILQSLALTWYSLSFIPFAR  
DAVKKCFAVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72

## FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCACTGGAGCAGCCACAGCAGGCCAACATGCTCTGCTGTGCCCTG  
TACGTGCCCGTCATCGGGAAAGCCCAAGCCAGACCGAGTTCCAGTACTTTCAGTCGAAGGGCTCCCTGCCAGCTGAAGTCC  
ATTTCAAGCTCAGTGTCTCATCCCCCTCCAGGAATTCTCACCTACCGCAGTGGAAAGCAGAAAATTGTCAGAAGCT  
GGAGATAAGGACCTTGATGGGAGCTAGACTTGAAGAATTGTCATTATCTCAAGATCATGAGAAGAAGCTGAGG  
CTGGTGTAAAGATTTGGACAAAAGAATGATGGACGATTGACGCCAGGAGATCATGAGTCCCTGCCGGACTTG  
GGAGTCAGATCTGAACAGCAGCAGAAAATTCTCAAGAGCATGGATAAAACGCCAGCATGACATCGACTGG  
AACAGTGGAGAGACTACACCTCTCACCCCTGGAAAATCCTCCAGGAGATCATCTACTGAAAGCATTCCACG  
ATCTTGATGGTGGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGGGAGCAGGGGATGTGGGAGA  
CACCTGGTGGCAGGAGGGGGAGGGGCGTATCCAGAACCTGCACGCCCTGGACAGGCTCAAGGCTCATG  
CAGGTCCATGCCATCCCGCAGCAACAACTGGCATCTGGTGGCTTCACTCAGATGATTGAGAAGGAGGGCCAGG  
TCACCTGGCGGGCAATGGCATACGTCCTCAAAATTGCCCCGAATCAGGATCAAATTCTAGGCCATATGAGCAG  
ATCAAGGCCCTTGTGGTAGTGAACAGGAGACTCTGAGGATTACAGAGGGCTTGCGCAGGGTCCCTGGCAGGGCC  
ATCAGGCCAGAGCAGCATCACCAATGGAGGCTGAAGACCCGGTGCAGGGCTGAGGAGCAGGCCAGTACTCAGGA  
ATGCTGGACTGCCAGGAGGATCTGGCAGAGAGGGGTTGGCCGCTTCTACAAGGGTATGTCCCAACATGCTG  
GGCATCATCCCTATGCCGGCATGCACCTGCACTGAGACGCTCAAGAATGCTGGCTGCAGCACTATGAGCTG  
AACAGGGGGACCCGGCTGTTTGCTCTGGCCTGTGGACCATGTCAGTAACCTGTGGCCAGTGGCCAGCTAC  
CCCCCTGGCCCTAGTCAGGACCCGGATGCAAGGCCAACGCTTATTGAGGGCTCTGGAGGTGACCATGAGCAGCCTC  
TTCAAAACATATCTGGCCAGGAGGGGCTTGGGCTGTAAGGGGCTGGCCCTTCTACAAGGGTATGTCCCAACATGCTG  
GCTGTGAGCATCAGCTAGTGGTCTACGAGAACCTGAGATCACCTGGCGTGCAGTCGGGTGACGGGGGGAGGGC  
CGCCCGCAGTGGACTCGTGTGATCTGGCCGAGGCTGGGTGCAAGGATCTCATTGTGAATGTGCCAACACT  
AACAGTCTCGAGCCAAGCTGTGAAAACCTAGACGCCACCCGAGGGAGGGTGGGAGAGCTGGCAGGCCAGGGCTT  
GTCCCTGCTGACCCAGAGACCCCTCTGGTCAAGGACGACATTCTCAGGCAAGGACACAGGCAATTCTTAGGGTCCAGGGTCAAGCAGG  
CTCCGGCTCACATGTGTAAGGACGACATTCTCAGGCTGGCCACGGGCTGCAAGGCTTGGGAGGCTCTGGGAGGCT  
TAGTTCTCCATTTCACCCCTGCAAGCAGCTGTTGGCACGGGCTCTGGCTCTGGCTGCACTCTCCCTGTG  
CCTCTGCTGCCTGCTGTGAGGTAAGGTGGGAGGGCTACAGGCCACATCCCACCCCTGTCACATCCC  
ATAATCATGATGAAAGGTGAGGTACGTGGCCTCCAGGCTGACTTCCAAACCTACAGGATTGACGCCAACATTGGC  
TGTGAAGGAAGGGAAGGATCTGGCTCTGGTCACTGAGCTGAGCCATCTGGGAGGCTCTGGGAGGCTCTGGGAGGCT  
CTTGGGAGTGCAGGGGCTCGGGCTGGCTGCAAGAGGAGCTGCTGGGGCTCATGGTCTCTGAGCT  
GGCCTGGACCCCTGTCAGGATGGGCCCCACCTCAGAACCAAACACTACTGTCAGTGGGAGGCTGGAGCA  
CCATGTTGAGGGCAAGGGCAGAGCTGGTGTGTTCTGGGGAGGGAAAGGAAAGGTGTTGGGAGGCTTAATTATGG  
ACTGTTGGAAAAGGGTTTGTCAGGACAGGACAAGGCCAGAACATGAGGGACTCTGTGCTTCCAGAGGAAGGCCAG  
GAGCAGGAGCTGGGACTGCTGAGCTGTTCTGAGGCTGGGGCTCTGCAACCCCCAGCAGGGGCCAGC  
GGGACCCACATTCTGTCAGGATGGGCCCCACCTCAGAACCAAACACTACTGTCAGTGGGAGGCTGGAGCA  
AACTATTATAGATTGTTAAATTAACTGCTGTCATTCTGAGGTTCTTGTGATGAGGTTATGCT  
GATTGTAACCTTCCAAAGCCGCCAGGGATGGGAGGAGGAGGAGGGGGCTGGGCGCTGAGTCACATCT  
GTCCAGAGAAATTCTTTGGGACTGGAGGAGAAAAGCCAGAACAGGAGCCAGCAGGCCCTGGCTCTTCTGGCAG  
GTTGGGGAGGGCTTGGGCCCCAGCTAGGATTTGAGGTTGACTGGGGCTGGAGAGAGAGGGAGGAAACCTCAAT  
AACCTTGAAGGTGGAATCCAGTTTCTCTGCGCTGGAGGGTTCTTATTCTCACTCTTCTGAATGTCAGGCAG  
TGAGGTGCGCTCTCACTGTAATTGTTGGTGGCGGGGCTGGAGGAGGGTGGGGGCTGGCTCCGTCCTCCAGC  
CTTCTGCTGCCCTGCTTAACAATGCCGCCACTGGCAGCTCACGGTTGCACTTCAATTCCACCAAGAATGACCTGA  
TGAGGAAATCTCAATAGGATGCAAGAGATCAATGCAAAATTGTTATATGAAACATATACTGGAGTCGTAAAAAG  
CAAATTAGAAGAATTGGACGTTAGAAGTGTCAATTAAAGCAGCCTCTAATAAAGTTGTTCAAAGCTGAAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLDG  
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNG  
TMTIDWNEWRDYHLLLHPVENIPEIILYWKHSTIFDVGENLTVDEFTVEERQTGMWWRHLVAGGG  
AGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIK  
FMAYEQIKRLVGSQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMILDCARR  
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTC  
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV  
VYENLKITLGVQSR

**Important features:**

**Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## **FIGURE 59**

GGAGGCAGCGGAGCTCCACTCAGCCAGTACCCAGATA CGCTGGAACCTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACACTGTCGCCTCAGCT  
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTGAACCTGACATCAAACCTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTAGGCTTGGTCCATGAGTCAGAAAGGCAAAGATG  
AGCTGTCGGAGCAGGATGAAATGTTAGGCTTGGTCCATGAGTCAGAAAGGCAAAGATG  
GGCAATGCCTTTGGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT  
CATCACCTCTAAAGGAAGGGAAATGCTAACCTTGAGTATAAAACTGGAGCCTCAGCATGCCGG  
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCCTGTGAGGCTCCCCGATGGTCCCC  
CAGCCCACAGTGGCTGGCATCCAAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATAC  
CAGCTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTCTGTGCTCTACAATGTTACGA  
TCAACAAACACATACTCCTGTATGATTGAAATGACATTGCCAAAGCAACAGGGATATCAAAGTG  
ACAGAACATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTCTGTGT  
CTCTTCTTCTTGCCATCAGCTGGCACTTCTGCCTCTAGCCCTTACCTGATGCTAAATTAAT  
GTGCCTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTCAC  
CACCAGATATGACCTAGTTATATTCTGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAAACAAGAGCAAGAAACAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAAT  
CTATCTCAAAGACATATTAGAAGTGGAAAATAATTCAATGTGAACTAGACAAGTGTGTTAAGA  
GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGAGTGAGAGGACAGGGATAGTGCATGTTCTGTCTGAATTTTAGTTATATGTGC  
TGTAAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCAACATATCCACATCTTATATCCAC  
AAATTAAGCTGTAGTATGTACCCCTAACGCGCTGCTAAATTGACTGCCACTCGCAACTCAGGGCG  
GCTGCATTTAGTAATGGGTCAAATGATTCACTTTATGATGCTTCAAAGGTGCCTGGCTTC  
TCTTCCAACTGACAAATGCCAAAGTTGAGAAAATGATCATAATTAGCATAAACAGAGCAGT  
CGGGGACACCGATTTATAAATAAACTGAGCACCTCTTTAAACAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 6o**

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS  
NTSFEILNSEVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKTESEIKRRSHLQLLNASKL  
CVSSFFAISWALLPLSPYLMLK

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

**N-myristoylation sites.**

amino acids 52-58, 126-132, 188-194

## **FIGURE 61**

TGACGTCAGAACATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAGGAGCCCCCTCCGGGTAGCTACTACCCCTGGACCCCCCAATAGTGGAGGGCAGTGGTAGT  
GGGCTACCCCCCTGGTGGTGGTTATGGGGGTCTGCCCTGGAGGGCCTATGGACCACCAGCTGG  
TGGAGGGCCCTATGGACACCCCCAATCCTGGATGTTCCCTCTGGAACCTCAGGAGGACCATATG  
GCGGTGCAGCTCCGGGGCCCTATGGTCAGCCACCTCCAAGTCTTACGGTGCCAGCAGCCT  
GGGCTTATGGACAGGGTGGCCCTCCAAATGTGGATCCTGAGGCCTACTCTGGTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTTCATTCAATGATGAGACCTGCCATGATGATAAACATGTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCACGGCTCTCAGCCCTGTGGAAATTATCCAGCAGTGGAAAGAACCTCTT  
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGCCC  
AAATGGGCTACAACCTGAGCCCCCAGTTCACCCAGCTCTGGTCTCCGCTACTGCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTGAGGACTTCGTCA  
CCATGACAGCTCTCGGATGCTATGACCCAACCATCTGTGGAGAGTGGAGTGCACCCAGGGACCTT  
TCCTGGCTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTCTGTCCCTAGAAGAAC  
ATTCTCCCTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATAGCCACCA  
AAATAGTGAGGACCGGGCTGAGGCCACACAGATAGGGCCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCCTGATGGCCATGAGCAGTTGAGTGGCAGCAGCTGGCACCAGGAGCAGGTCTTGTAAATGG  
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCCTGATGCCAGTGGTAGTGTCTGCCCTGTACCC  
GTTAGTACCTGTGTTCCCTCACCGGCCATCTGTCAAACGAGCCATTCTCCAAAGTGGAAAT  
CTGACCAAGCATGAGAGAGATCTGTCTATGGACCAGTGGCTGGATTCTGCCACACCCATAAAAT  
CCTTGGCTGTAACTCTAGCTGCCCTGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGCAT  
CTTGGCCAGGCTCTGCCCTGCAGCTGGACCCCTCACTTGCCCTGCCATGCTCTGCTCGGCT  
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTAATTGCATTTTTTC  
ATTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSPGTGGPYGGAAPGGPYGQPPPSSYGAQQPGLYQGGAPPNVDPEAYSWFQSVDSDH  
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSAWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQLVLTAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

## **FIGURE 63**

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGCTGTCTTCATC  
TCCCAGGCCTCTTGCCCCGGAGCATCGGTGTTGAGGAGAAAGTTCCAAAACTTCGGGACC  
AACTTGCCCTCAGCTCGGACAACCTCCTCCACTGGCCCTCTAACTCTGAACATCCGCAGCCC  
TCTGGACCCTAGGTCTAATGACTTGGCAAGGGTCTCTGAAGCTCAGCGTGCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGCTGCCTGCCATG  
GATTCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGCTGAGGACCGCCTGGGG  
AGCGCTGCCTAAGAAACTCTTACCTCTCCAGTGCTGCGCCCTCGCTCCGGCAGTGGCCTT  
TGCCTGGGGAGTCTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCGTTCTAATTCACTGGAGCCGGGGAAAATCCTTCCAAACG  
CCCTCCCTGGTCTCATCCACAGGGTTCTGCCTGATACCCCTGGGTACCCTGAATCCAGTG  
TGTCTGGGGAGGTGGAGGCCCTGGGACTGGTGGGGAACGAGGCCATGCCACACCTGAGGGA  
ATCTGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGAAATATTAATCGGTATCCAGGAGG  
GCAGCTGGGGAAATATTCATCTACCCAGGTATCAATAACCCATTCCTCTGGAGTTCTCCGC  
CCTCCTGGCTCTTGGAAACATCCCAGCTGGCTCCTAATCCTCCAAGCCCTAGGTTGCAGTG  
GGGCTAGAGCACGATAGAGGGAAACCCAACATTGGAGTTAGAGTCCTGCTCCGCCCTTGCTG  
TGTGGCTCAATCCAGGCCCTGTTAACATGTTCCAGCACTATCCCACTTTCAGTGCCTCCCC  
TGCTCATCTCCAAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AA

## **FIGURE 64**

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAEDRLGEA  
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRLPRSNSILGAGGKILSQRP  
PWSLIHRVLPDHPWGLTNPSVSWGGGGPGTGWGTRPMPHPEGIWINNQPPGTSGWNINRYPGGS  
WGNINRYPGGSGWNINRYPGGSGNIHLYPGINNPFPVGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCATCCCAGGAGCGCAGTGGCCACTATGGGTC  
TGGGCTGCCCTTGTCCCTCCTGACCCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTGCAACTGAAGCTGAAGGAGTCTTCTGACAAATTCCCTCATGAGTCCAGCTCCTGGAA  
TTGCTTGAAAAGCTCTGCCTCCCTCCATCTCCCTCAGGGACCAGCGTCACCCCTCCACCATGC  
AAGATCTCAACACCATGTTGTCGAACACATGACAGCCATTGAAGCCTGTGCCTTCTGGCCC  
GGGCTTTGGGCCGGGATGCAGGAGGCAGGCCCCGACCCGTCTTCAGCAGGCCCCCACCTC  
CTGAGTGGCAATAAAATTGGTATGCTG

## **FIGURE 66**

MGSGPLVLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSGTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## **FIGURE 67**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCGGC  
CAGGTGCCCGTCGCAGGTGCCCTGGCCGGAGATGCGGTAGGGGGCGAGCGCGAGAACCCCC  
TTCCTCGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGCTGCTTCTGGCG  
CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCGAGCCTGGGGCAAATACAGACCACCTCTGC  
AAATGAGAATAGCACTGTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTGGCTGCCCTGCTCCTGGCTGTGGGCTG  
GCACTGTTGGTGGGAAGCTTCGGGAGAACGGGAGACGGAGGGACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCCATGCAGCCGAGGCCGGCCCTCAGGACTCCAAGGAGACGGTGAGGGCT  
GCCTGCCCATCTAGGTCCCCTCTGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAAGGTA  
AGACTCTGCCCTGAGGTCAAGAGAGGATGGGCTATTCACTTTATATATTATATAAAATTAG  
TAGTGAGATGTAAAAAAAAAAAAAA

## **FIGURE 68**

MANPGLGLLLALGLPFLARWGRAWGQIOTTSANENSTVLPSSSSDGTLRPEAITAIIVVFS  
LLAALLLAVGLALLVRKLREKQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32

**FIGURE 69**

## **FIGURE 70**

MGLFRGFVFLVLCLLHQSNNTSFIKLNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTASTYLFE  
ATEKRFKKNVSIILIPENWKENPQYKRPKHENKHADVIVAPPTLPGRDEPYTKQFTECGEKG  
EYIHFTPDLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRC  
SAGISGRN  
RVYKCOGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDS  
VVEFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSG  
SMGGKDRLN  
MNQAAKHFLLOQTENGWSWGMVHFSTATIVNKLIQIKSSDERNTLMAGLPTYPLGG  
TSICSGIK  
YAFQVIGELHSQLDGSEVLLTDGEDNTASSCIDEVKQSGAIVHFI  
ALGRAADEAVI  
EMSKITGG  
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDT  
VIIDSTVGKDTFFL  
ITWNSLPPSISLWDPSGTIMENFTV  
DATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITV  
TSR  
AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYV  
FVLGANV  
TAFIESQNGHTEV  
LELLDNGA  
GADSFKNDGVYSRYFTAYTENGRYSLKVR  
AHHGGANTARLKLRP  
PLNRAAYIPGWVV  
NGEIEANPP  
RPEI  
DEDTQTTLED  
FSRTASGGAFV  
VSQV  
ESLPLPDQYPP  
SQITD  
LDATV  
HEDKII  
LTWT  
APGDN  
FDVGKVQRYIIRISAS  
ILDLRDSFDDALQVNT  
TDLSP  
KEANSKES  
FAFK  
PENISE  
ENATHIFIA  
KS  
IDKSNL  
TSKV  
SNIA  
QV  
TLF  
IPQANP  
DDID  
PTPT  
PT  
PDK  
SHNS  
GVN  
IST  
LVL  
SVI  
GSV  
VNI  
FIL  
STTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## **FIGURE 71**

CTCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGGCAGGGGTGA  
CAACAGGTGTCATCTTTGATCTCGTGTGGCTGCCCTCTATTCAAGGAAGACGCCAAGGTAAAGGCA  
GAGGAGCAATGATGTAGCCACCTCTAACCTCCCTCTTGAAACCCCAAGTATGCCAGGATTACTAGAGTGTCA  
ACTCAACCAAGCGCTCTCGGCTTAACCTGTGGTTGGAGAGAACCTTGTGGGGCTGCGTCTTAGCA  
GTGCTCAGAAGTGAATTGCTGAGGGTGGACCAGAAGAAAGGAAAGGTCCTCTGCTTGGCTGCCACATCAGGAA  
GGCTGTGATGGGAATGAAGGTAAGGAACTTGAGATTCACTTCAGTCATTGCTTGCTGCCAAGATCATCCTTAAA  
AGTAGAGAAGCTGCTCTGTGTGGCTAGCCAGAGCTGGTCAAGGAAATGGATGCAAGCAGCTC  
CGGGGCCCCAAACGCTGCTCTGTGGCTAGCCAGGCGCCCTCCGTGGGGCCGGCTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTATTCTGAATGATGATGGTCGCGGGGCTGCTTGCGTGGATTCCGGGTGGT  
GTTTGCTGGTCTCTGCTGTGCTATCTGTGCTGTACATGTTGGCTGACCCCAAAGGTCAGCAGGAGCAG  
CTGGCACTGCCCCAGGGCAACAGCGGACAGGGTACAGGGCTGAGGAGGAGTGGGAGGAGCAG  
CGCAACTACGTGAGCAGCTGAAGCGAGATGCCACAGCTCAAGGAGGAGCTGAGGAGGAGTGA  
AATGGGCAGTACCAAGGCCAGCGATGCTGCTGGCTGGCTGAGGAGCCAGGCCCCAGAGAAAACCCAGGCCACCTC  
CTGGCTTCTCTGCACTCCAGGTCAGGCAAGGAGGTGAATGCTGGCTCAAGCTGGCCACAGAGTATGCAGCAGTG  
CCTTCGATAGCTTACTCTACAGAAGGTGTACAGCTGGAGACTGGCTTACCCCAACCCGGAGGAGAACGCTGTG  
AGGAAGGACAAGGGGATGAGTTGGAGAACATTGAATCAGGCTTGGAGACCTGAACAAATCTGCAGAGAACAGC  
CCCAATCACCGCTCTTACACGGCTCTGATAGGAGTACCGAACAGAACAGGACATTGTAT  
GAGCTCACCTCAAGGGACCAACAAACAGAATTCAACAGCTCATCTTATTGACCATTCAGCCCCATCATGAAA  
GTGAAAATGAAAAGCTAACATGCCAACACGCTTACATGTTATGTCGCTCTAGCAAAAGGGTGGACAAGTTC  
CGGCAGTCTAGCAGAATTCAAGGGAGATGTGATTGAGCAGGATGGGAGAGTCATCTACTGTTGTTACTTGGG  
AAAGAAGAATAATGAAGTCAAAGGAATCTGAAACACTTCAAAAGCTGCCAACACTTCAAGGAACTTACCTTCATC  
CAGCTGAATGGAAATTTCAGCTGCTGAGGACTTCTGATGTTGGAGCCGCTCTGGAGGGAAAGCAAGTCCCTCTC  
TTTTCTGTGATGGACATCTACTTCACATCTGAATCTCAATACGTCAGGCTGAATACACAGCAGGGAAAG  
GTATTCTCATCCATTCTCAGTCAGTACAATCTGCCATAATATACGGCCACCATGTCAGTCCCTCCCTGGAA  
CAGCAGTGGCTATAAGAAGGAAACTGGATTGGAGAGACTTGGATTGGGATGACGTGTCAGTATCGTCAGAC  
TTCATCATATAGTGGTTGATCTGGACATCAAAGGCTGGGGAGAGGATGTCACCTTATCGCAAGTATCTC  
CACAGCACCTCATAGTGGTACGGACGCCGTGCGAGGACTCTTCACCTCTGGCATGAGAACGGCTGCATGGAGG  
CTGACCCCCGGAGCAGTACAAGGATGTCATGCCAGGCTACCTGCCAAACAGAACAGAACAGTAGC  
GAAGGATTGTGGGGACACTTTTCTTCCTTGCATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA  
GGACGACAAAAGAATTGGACTGATGGCTAGAGATGAGAAAGGCCGCTTCTGTGGCTTACACAGA  
AATCAAATCTCGCTTCTGCATAAGGAAACCTGGTACCTGACCTTGTGAAAGTGTGACAAAGGAGAACATGCTTG  
AGATTATAAGCTAATGGTGGAGGTTGATGGTTACATCAACTGAGACCTGGTACCTGTTGTTGTGCTCATG  
AATATTCAATGATTAAAGAGCAGTTTGTAAAATTCATTAGCATGAAAGGCAAGCATATTCTCTCATATGAATGA  
GCCTATCAGCAGGGCTCTAGTTCTAGGAATGCTAAATATCAGAAGGCAAGGAGAGGAGATGGCTTATTGATACT  
AGTGAGTACATTAAGTAAAATAAAATGGACAGAACAGAACCATAAATATGTCATATTCCCCAAGAT  
TAACCAAAAATACTGCTTATCTTTGGTGTCTTTAACTCTCTGTTTATTAAATGACT  
TTTTCTCTTACAGGAGGAAACTCATTGAGACTTCTGATGTTACATCTGAGGACACTTGTGAAAGCACAAGTGGCCTAC  
ATTTTATATTCTTAAGAAGATACCTTGAGATGCAATTGAGACTTCAAGGATCAAATTGATGCCATAT  
CCAAGGACATGCCAAATGCTGATTCTGTCAGGCACTGAATGTCAGGCACTGAGACATAGGGAGGAATGGTTGTA  
AATACAGACGTACAGACTTTCTGAAGAGTATTCTGAAGGAGGCAACTGAACACTGGAGGAAAAGAAAATGAC  
ACTTTCTGCTTACAGGAGGAAACTCATTGAGACTTCTGATGTTACCTAAAGTCAAGAACACATT  
CTCCTCAGAAGTAGGGACCGCTTCTACCTGTTAAATAACCAAGTACCTGAGGACATGTCAGGCTGAA  
AAAACAGGGTGCTCTCTGCTTCTGCTTCAAGAAGAAATGGAGAAAATATATATATATATATATTGT  
GAAAGATCAATCCATGCGAGAATCTAGTGGGAGGAAAGTTTGCTACATGTTATCCACCCAGGCCAGGGAG  
TAACTGAATTATTCTTAAATTAAAGCAGTTCTACTCAATCAGGAGGAGTGTGAAAGTATTGACATT  
CAAACATTTAAAATACAGTAAACATAAGTGGTTCTCATTGCTGAAAGTATTGACATT  
ATGCATGAGCTAATTATCTCTTGGCTTGTGCTTCAAGTAAACCTATTGTTAAAAGCTTCAAGAAC  
ATTCAAGCTGGTGGTGTGTTAAAATGATTGATTTGACTGGTACTTTATGAAATTAAACACAGG  
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATGATTGTGGATATGAA

## **FIGURE 72**

MMMVRRGLLAWISRVVVLLVLLCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWE  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIESALETLNNPA  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLMAN  
TLINIVPLAKRVDKFQFMQNREMCEQDGRVHLTVYFGKEEINEVKGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFQSQY  
NPGIITYGHDAVPPLEQQLVIKKETGFWRDFGFGMTQCQYRSDFINIGGFDDIKGWGGEDVHLYR  
KYLHSNLIVVTPVRGLFHLWHEKRCMDELTPEQYKMCMQSKAMNEASHGQLGMLVFRHEIEAHL  
RKQKQKTSSKKT

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 315-319, 324-328

**N-myristoylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

**Amidation site.**

amino acids 377-381

## **FIGURE 73**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGAGTTGTCTGGGATCCA  
GAAACCCATGATACCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGA  
GAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCACTCCTC  
CCTCCCTCTCTCTGCTGTCTAGTCCTAGTCCTCAAATTCCAGTCCCTGCACCCCTTC  
CTGGGACACTATGTTCTCCGCCCTCTGCTGGAGGTGATTGGATCTGGCTGCAGATGGG  
GTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATGGCCAGCCTCTTACCCGTAGTGT  
GGAAACAAATGCCAGTCGCCATCGATATTCAAGACAGACAGTGTGACATTGACCCGTATTGCC  
TGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTGGACCTGCACAACAATGCC  
ACACAGTGCAACTCTCTGCCCTCTACCCGTATCTGGGTGACTCCCCGAAAATATGTAGCT  
GCCAGCTCCACCTGCACTGGGTCAAGAAAGGATCCCCAGGGGGTCAGAACACAGATCAACAG  
TGAAGCCACATTGCAAGACTCCACATTGTACATTATGACTCTGATTCTATGACAGCTTGAGTG  
AGGCTGCTGAGAGGCCTCAGGGCCTGGCTGTCCTGGCATCCTAATTGAGGTGGTGAGACTAAG  
AATATAGCTTATGAACACATTCTGAGTCACCTGCATGAAGTCAGGCATAAAGATCAGAACACCTC  
AGTGCCTCCCTCAACCTAACAGAGAGCTGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATG  
GCTCGCTCACAACTCCCCCTGCTACCAAGAGTGTGCTCTGGACAGTTTTATAGAAGGTCCAG  
ATTCAATGAAACAGCTGAAAAGCTCAGGGACATTGTTCTCCACAGAGGAGCCCTCTAA  
GCTTCTGGTACAGAACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTTGCTCTTCA  
TCCAAGCAGGATCCCTGTATACCACAGGTGAAATGCTGAGTCTAGGTGTTAGGAATCTGGTTGGC  
TGTCTCTGCCTCTCTGGCTGTTATTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAA  
CCGAAAGAGTGTGGCTTCACCTCAGCACAAGCCACGACTGAGGCATAAAATTCCCTCTCAGATA  
CATGGATGTGGATGACTTCCCTCATGCCTATCAGGAAGCCTCTAAATGGGGTAGGATCTGG  
CCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTCTTAGAGAGGAAT  
GGACCCAGGCTGTCATTCCAGGAAGAAGACTGCAGAGCCTCAGCCTCTCAAACATGTAGGAGGA  
ATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTGTGTTAGTGCAGGGAAAGTTGG  
ATATACCCCAAAGTCCCTACCCCTCACTTTATGGCCCTTCCCTAGATATACTGCGGGATCT  
CTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGATATTTGATCAATATAATTGGAAATTAAAG  
TTTCTGACTTT

## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSTFDPLPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEAT  
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTLFSTEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## **FIGURE 75**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGACGGGCAGTCCCTGTGCT  
TCTGGGGTTGCCAACCTGCAAACATCACCTCTTATCCATCAACATGAAGAATGCCTACA  
ATGGACTCCACCAGAGGGCTTCAGGAGTTAAAGTTACTTACACTGTGCAGTATTCATCACAA  
ATTGGCCCACCAGAGGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTGCTGACAGCTCC  
AGAGAAGTGGAAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTGAATACTAAACAAACAGAACGTGGTCCCAGTGTGACCAACCAC  
ACGCTGGTGCACCTGGCTGGAGCCGAACACTCTTACTGCGTACACGTGGAGTCCTCGTCCC  
AGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTGCCAGGACTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTGCCTATCTATTACCGTGTTCCTTTT  
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATT  
GATTTGATTATGGAAATGAATTGACAAAAGATTCTTGTGCCGTGCTGAAAAAAATCGTGATTA  
ACTTTATCACCCCTCAATATCTCGGATGATTCTAAATTTCTCATCAGGATATGAGTTACTGGGA  
AAAAGCACTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCTCAGGA  
GGAAGAGGAGGTGAAACATTAGGTATGTTGCATTTGATGGAATTGGACTCTGAAG  
AAAACACGGAAGGTACTTCTCTCACCCAGCAAGACTCCTCAGCAGAACAAATACCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTGCGGGGCTGAAGAGCAGGA  
GCTCAGTTGCAGGAGGTGTCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG  
TCCTGGGCCGAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGGA  
TCCCCAAACTGGCAGGCTGTGATTCCCTCGCTGCTCAGCTCGACCAGGATTAGAGGGCTGCG  
AGCCTCTGAGGGGATGGGCTGGAGAGGGTCTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCCAGGAGAAAATGAAACCTATCTCATGCAATTCTATGGAGGAATGGGGTTATA  
TGTGCAGATGGAAACTGATGCCAACACTCCTTTGCCCTTGTGCAAACAAAGTGAG  
TCACCCCTTGATCCCAGCCATAAGTACCTGGGATGAAAGAAGTTTCCAGTTGTCACTGAG  
CTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTGGTTATGCATGTA  
GGTCTTAACAATGATGGTGGCCTCTGGAGTCAGGGCTGGCCGGTTGTTATGCAGAGAA  
AGCAGTCATAAAATGTTGCCAGACTGGGTGAGAATTATTCTAGGTGGGTG

## **FIGURE 76**

MSYNGLHQRFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDKRFFVPAEK  
IVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHTMLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSILQEEVSTQGTLLESQA  
ALAVLGPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSILSSFDQDS  
EGCEPSEGDSLGEGLLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQMen

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## **FIGURE 77**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGACTTGCTGCCCTGACAC  
CTGGGAAG**A**TGGCCGGCCCGTGGACCTTCACCCCTCTCTGTGGTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTGAACACCGTCCTGAAGCACATC  
ATCTGGCTGAAGGTCACTCACAGCTAACATCCTCCAGCTGCAGGTGAAGGCCCTGGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATCCGATGGACACCAGTGCAAGTGGC  
CCCACCCGCGCTGGTCCTCAGTGAATGTGCCACCAGCCATGGGAGCCTGCGCATCCAATGCTGTA  
TAAGCTCTCCCTGGTGAACGCCCTAGCTAACAGGTCAAGCAGGTATGAAACCTCTAGTGCCATCCCTGC  
CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGGCTCCCTCAATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCATTCCCTCAGCATTGACCGTCTGGAGTTGACCTCTGTA  
TCCTGCCATCAAGGGTACACCATTCACTACCTGGGGCCAAGTTGGACTCACAGGGAA  
AGGTGACCAAGTGGTCAATAACTCTGCAGCTCCCTGACAATGCCACCCTGGACAACATCCCG  
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGAGCTGCACTGGCTGCTGTCTCTCCAGAAGA  
ATTCACTGGTCCCTGGACTCTGTGCTTCTGAGAGTGCCATCGCTGAAGTCAGCATCGGC  
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTAAGATCTTAACACTCAGGAC  
ACTCCCGAGTTTTATAGACCAAGGCCATGCCAAGGTGGCCAACGCTGCTGGAGTTGTT  
TCCCTCCAGTGAAGGCCCTCCGCCCTTGTTCACCCCTGGCATCGAAGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAGGTGACCAACTTAACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG  
ATGAACCTCTGGGATGGCTGGTCCAACCTGATGTTCTGAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGGTCCCAGTGTCAATTGGTGAAGG  
CCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCCAGCCTCC  
TTGTGGAAACCCAGCTCTCTGTCTCCAGT**G**AAGACTTGGATGGCAGCCATCAGGGAAAGGCTGG  
GTCCCACTGGAGTATGGGTGTGAGCTATAGACCATCCCTCTGCAATCAATAAACACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPVKIKEKLTQELKDHNATSILQQLPLLSAMREK  
PAGGIPVLGSLVNTVLKHIIWLKVITANIQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLQLQVLPVISLISIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQGKVT  
KWFNNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPPEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEALRPLFTLGEASSEAQFYT  
KGDQLILNLNNISSLRQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSLVKALG  
FEAAESSLTKDALVLTPASLWKSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## **FIGURE 79**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACTTGTGGCTACATCCTAGGCCTCTGGGGCTTTGGGCACACTGGTTGCCAT  
GCTGCTCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATGGTACAGCAGTTGGCTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC  
ACCCCTCTGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGATGGTACATCCAGTGAAT  
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCCAGTCTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTCATCCTGGAGGCCCTGGGATTC  
ATTCCCTGTTGCCTGGAATCTCATGGGATCCTACGGGACTCTACTCACCACGGTGCCTGACAG  
CATGAAATTGAGATTGGAGAGGCTCTTACTTGGGATTATTCTCCCTGTTCCCTGATAG  
CTGGAATCATCCTCTGCTTCTGCTCATCCCAGAGAAATCGCTCCAACACTACGATGCCCTAC  
CAAGCCAACCTCTGCCACAAGGAGCTCTCCAAGGCCCTGGTCAACCTCCAAAGTCAAGAGTGA  
GTTCAATTCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGTGGCTG  
GGTCTGTGAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCAACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG  
GCTAGTGTAAACAGCATGCAGGTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTTCC  
TCACCTGCTGCTCCCTGCCCTAAGTCCCAACCTCAACTGAAACCCATTCCCTTAAGCCA  
GGACTCAGAGGATCCCTTGGCCCTGGTTACCTGGACTCCATCCCAAACCCACTAATCACA  
TCCCACGTGACTGACCCCTCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCACTCTGTTATGACTCCACAGTGTCCA  
GACTAATTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

## **FIGURE 80**

MASLGLQLVGYILGLLGLLGTIVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSIASSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNLHGILRDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

## **FIGURE 81**

CCCCACCGCGTCCGCCTCTCCCTCTGCTGGACCTTCCCTCGTCTCCATCTCTCCCTCTTC  
CCCCCGTTCTCTTCCACCTTCTCTTCCACCTAGACCTCCCTCCCTGCCCTCTTCC  
GCCCACCGCTGCTTCCCTGGCCCTCTCCGACCCCGCTAGCAGCAGACCTCTGGGCTGTGG  
GTTGATCTGTGGCCCTGTGCCCTCGTCTCCCTCCGACTCCGCTCCGG  
ACCAGCGGCCTGACCTGGGGAAAGGATGGTCCCGAGGTGAGGGCTCTCCCTGCTGGGA  
CTCGCGCTGCTCTGGTCCCCCTGGACTCCACGCTCGAGCCGCCAGACATGTTCTGCCTTT  
CCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT  
ACTGCCCTGCGCTGTACCTGCTCAGAGGGGCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT  
GTCCACTGCCCTCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTTGGAACCTCACAC  
TCCCTCTGGACTCCGGCCCCACCAAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG  
AGATCTTCAGTGCCTATGAGCTGTTCCCTCCCGCTGCCCAACCAGTGTGTCCTCTGCAGCTGC  
ACAGAGGGCCAGATCTACTGCCCTCACAAACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCC  
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGTGCTGGAGAAAG  
AGAGGCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTCATCCCTGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATGTCCTGAAGGAGAAACATAAGAAAGCCT  
GTGTGCATGGCGGAAGACGTACTCCACGGGTGTGGCACCCGGCTTCCGTGCCTTCGGC  
CCCTGCCCTGCATCTATGCCCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCAGAG  
ACAAAGCAGCCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTC  
CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCCGTGCTTGCCTGGAACACGAGGC  
CTCGGACTTGGTGGAGATCTACCTCTGGAAAGCTGGTAAAAGATGAGGAAACTGAGGCTCAGAGAG  
GTGAAGTACCTGCCCAAGGCCACACAGCCAGAATCTTCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
GGAACGTCTCCATTGCCAGACCCCTGGAGCTGAAGGTACGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATTAATAAA  
TAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELP  
PSRLPNQCVLCSCTEGQIYCGLTTCEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPGTAPGTLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKACVHGGKTY  
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLSDQESQEARNLPERGTALPTARWPPRSLERLPSDPGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## **FIGURE 83**

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTACGCAGAGCCTCTCC  
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCCTTCTCTAATCCATCCGTACCTCTCCTGTCA  
TCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTGGTTCTGAGTC  
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTGGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAG  
GACGCAGCATTCTCCTGTTCTGCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGGTTCTCAGGGG  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGCAGGGAGGACCAGCCATTATGCAGATGCCACAGTAC  
AAGGCAGGACAAAATGGTGAAGGATTCTATTGGGAGGGGCGATCTCTGAGGCTGGAAAACATTACT  
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTACTACCAGAACGGCATCTGGAGCT  
ACAGGGTGCAGCACTGGCTCAGTTCTCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCAGTCCTCGGGCTGGTCCCCCGGCCACAGCGAAGTGGAAAGGTCACAAGGACAGGATTGTC  
ACAGACTCCAGGACAAACAGAGACATGCATGGCTGTTGATGTGGAGATCTCTGACCGTCCAAGAGAA  
CGCCGGAGCATATCTGTTCCATGGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG  
GAGATACCTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGAAACTCTGCTGTGGCTA  
TTTTTGGCATTGTTGACTGAAGATTTCTTCCAAATTCCAGTGGAAATCCAGGCGGAACGGACT  
GAGAAGAAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAG  
AGACGGCTCACCCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATAGAAAAGCTCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCTCTCAGAGTTCCAAGCAGGGAAACATTA  
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTGTCTCCGATCATGGTACTGGTCTCAGACTGAATGGAGAACATTGTATTTC  
ACATTAATCCCGTTTATCAGCGTCTCCCCAGGACCCACCTACAAAATAGGGTCTCTGGACTA  
TGAGTGTGGGACCATCTCCTCTTCAACATAAAATGACAGTCCCTTATTATACCCCTGACATGTCGGTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAATGAACTCCCATAGTCATCTGC  
CCAGTCACCCAGGAATCAGAGAAAAGAGGCCCTCTGGCAAAGGCCCTCTGCAATCCCAGAGACAAGCAACAG  
TGAGTCCTCCTCACAGGCAACCACGCCCTCCCTCCCCAGGGTGAATGTAGGATGAATCACATCCCACAT  
TCTTCTTCTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCAAGGTGGCTTCCA  
GATGAAGGGGACTGCCGTGTCACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGAGGAAGAAGG  
CTGACATTACATTAGTTGCTCTCACTCCATGGCTAAGTGTGATCTGAAATACCACCTCAGGTGAAG  
AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGTATCTAATGGTTGTTCAATTATATTACACTTCAAGTAAAAAA

## **FIGURE 84**

MALMLSIVSLLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSSVH  
LYRDGKDQPFMOMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQKAIWELQ  
VSALGSVPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPOGQDLSTDRTNRDMHGLFDVEISL  
TVQENAGSISCSMRRAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAEQELDWRRKHGQAEQELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQSFOAGKHYWEVDGGHNKRWRVGVCRDDVDRKEYVTLSPDHGYWVRLNGEHLYFT  
LNPRFISVFPRTPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPETSNSSESSSQATTPFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

## **FIGURE 85**

AACAGACGTTCCCTCGGGCCCTGGCACCTAACCCAGACATGCTGCTGCTGCTGCCCT  
GCTCTGGGGAGGGAGAGGGCGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCTACCCCTCGCATGGCTGGATT  
TACCTGGCCAGTAGTTCATGGCTACTGGTCCGGAAAGGGCCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTGGCAGTGTGGAGGAGACTGGGACCGATTCCACCTCTTG  
GGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGAAGTGTGATGCCGGAGA  
TACCTCTTCGTATGGAGAAAGGAAGTATAAAATGAAATTATAAACATCACCGGCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCAGGCACCCCTGGAGTCCGGCTGCC  
AGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCAACCCGCTCCTCGGTGCTACCCCATCCCACA  
GCCCGAGGACCATGGCACCAGCCTCACCTGTCAAGGTGACCTCCCTGGGGCCAGCGTGACCACGA  
ACAAGACCGTCCATCTAACGTGCTCACCGCCTCAGAACCTGACCATGACTGTCTCCAAGGA  
GACGGCACAGTATCCACAGTCTGGAAATGGCTCATCTGTCACTCCCAGAGGGCCAGTCT  
GCGCCTGGTCTGTGCAAGTTGACAGCAACCCCTGCCAGGCTGAGCCTGAGCTGGA  
GAGGCCTGACCCCTGTGCCCTCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCCTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCCTCGGCTCTCAGCAGGTCTACCT  
GAACGTCTCCCTGCAGAGCAAAGCACATCAGGAGTGAACAGTCAGGGGTGGTGGAGCTGGAG  
CCACAGCCCTGGTCTTCCTGTCCCTCGGTATCTCGTTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGAGATACGGCATAGAGGATGCAAACGCTGTCAGGGTTC  
AGCCTCTCAGGGGCCCTGACTGAACCTGGCAGAACAGACTCCCCCAGACCAGCCTCCCCAG  
CTTCTGCCCGCTCCAGTGGGGAGAGGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG  
AAGCCTGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCA  
GAGGCTGATTCTTGTAGAATTAAACAGCCCTAACGTGATGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAGAACACAGGCTTAGAGTCAAAGTATCTAAACCTGAATCCACACTGTGCC  
TCCCTTTATTTTTAACTAAAAGACAGACAAATTCTTA

## **FIGURE 86**

MLL LLL PLL WGR ERA EG QTS KLL TMQ SS VTV QEG LCV H VPC SF SY PSH G WI Y PGP VV H GY W FREG  
A NT D QD A P V A T N N P A R A V W E E T R D R F H L L G D P H T K N C T L S I R D A R R S D A G R Y F F R M E K G S I K W N Y  
K H H R L S V N V T A L T H R P N I L I P G T L E S G C P Q N L T C S V P W A C E Q G T P P M I S W I G T S V S P L D P S T T R S  
S V L T L I P Q P Q D H G T S L T C Q V T F P G A S V T T N K T V H L N V S Y P P Q N L T M T V F Q G D G T V S T V L G N G S S L  
S L P E G Q S L R L V C A V D A V D S N P P A R L S L S W R G L T L C P S Q P S N P G V L E L P W V H L R D A A E F T C R A Q N P  
L G S Q Q V Y L N V S L Q S K A T S G V T Q G V V G G A G A T A L V F L S F C V I F V V V R S C R K K S A R P A A G V G D T G I E  
D A N A V R G S A S Q G P L T E P W A E D S P P D Q P P P A S A R S S V G E G E L Q Y A S I S F Q M V K P W D S R G Q E A T D T E  
Y S E I K I H R

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

## **FIGURE 87**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGAGTGGAGGGAGGTGAAGGAGCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTTT  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAGGAATGGACCTGT  
TCTTCGTCTCCATCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA  
TGGCCTGTATTTCTCCGCACTGAGAATGGTGTATCTACCAAGACCTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGAGTGCACGGTG  
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGACGGCAACTGGGC  
CAACTACAACACCTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTGCCAATAAGTCCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGAGGTACCGCACGGACACTGGCTCCTCCAGACACTGGGACATAATCT  
GTTTGGCATCTACCAGAAATATCCAGTGAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC  
CGGTGATCCCTGTGGCTATGATTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCCAT  
GGCCAGCGGAATTCACTGCGGGATTGTTAGTCAGGTACGGTATTTAATAACGAGAGAGCAGCCAA  
CGCCTTGTGTGCTGGAATGAGGGTACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTCCAGAGGCCAGTCCCAGCAGTGTGGAGATTTCTGGTTTGATTGGAGTGGATAT  
GGAACTCATGTTGGTTACAGCAGCAGCGTGAAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
**TTGAGAG**TTTGTGGAGGGAAACCCAGACCTCTCCACCAGATGAGATCCAAAGGATGGAGAA  
CAACTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRSSQQGSKADYPEDGDNWANYNTFGSAAAT  
SDDYKNPGYYDIQAKDLGIWHVPNPKSPMQHWRNSSLRYRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTNDNGPVIKVYDFGDAQKTASYYSPYQOREFTAGFVQFRVFNNERAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristoylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## **FIGURE 89**

CTAGATTGTCGGCTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGTCTCAGGGCTTGTGCCCTCGCTTCTGACG  
CTCCTGGCGCATCTGGTGGTCGTATCACCTTATTCTGGTCCCAGGACAGCAACATACAGGCTG  
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCT  
CTGTCACCCCTGGGCCCTTTGCAGTGGAGCTGGCCGGTTCCCTCTCAGGAGTCTCATGTTAAC  
AGCACCCAGAGCCTCATCTCATTGGGCTCACTGTAGTGCATCCGTGGCCCTGCTCTTCTCAT  
ATTGAGCGTGGGAGTGCACTACGTATTGGTACATTGGTCTGCAGTGCCCTCCAGCTG  
TCACTGAAATGGCTTATTGTCACCGTCTTGGGCTGAAAAAGAAACCCTCTGATTACCTTC  
TGACGGAACCTAAGGAGCAAGCCTACAGGGCAAGGGCGCTCGTATTCCCTGGAAGAAGGAAG  
GCATAGGCTCGGTTTCCCTCGAAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG  
TCTTGAGTCTGGGATTATCCGCATTGTATTAGTGCCTTGTAAATAATGTTGAGTAACA  
TTAAGACTTATACAGTTTGGGACAATTAAAAAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFC SALPAVTEMALFV  
TVFGLKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

## **FIGURE 91**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACCGAGAGCGGGAGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTATCTGGTCATCTGTGGCCAGGATGATG  
GTCCTCCGGCTCAGAGGACCCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCCCTGGGGAGGCTTGGGCATTCTGGCAGCCCCCAACCGCCCCGAACCACAGCCCC  
CACCCCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGGCAGTCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGGAAAGATTGTGGACCATGGCAATGGACCTTCAGCGTCCACT  
CCAACACAATGCCACAGGCCAGGGAAACATCTCATCAGCCTCGTCCCCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTCATCGAAGCCAAGGCCTCCAAAATCTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGCCGCCGACCTCGCTTGCACCCACGACCCAGCCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTCAAAGTCGTCTGTG  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAAC  
CATAGTGTATAACCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGGC  
TGGAAAGGACAGGCCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAAGGGTTGGGCTC  
AGGCAGGGAGGGGGGGTGGAGACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCAAGTGTGGTCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGCTCTGTGAGCCACAGGGCTTGCCACGGAGCCACAGAGAGATGCTGG  
TCCCCGAGGCCCTGTGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAAGC  
CCTTGGTTCTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGAGATTCATCAGTGTGGACA  
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTCCTAGGAGCCAGTCAGCAGGGTGGGGTGG  
GCCAGAGGAGCTCCAGCCCTGCCCTAGTGGGCCCTGAGCCCCCTGTGCTGTGAGCATGG  
CATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGCTTGACAGATTGACCACCTGTCTCCAGC  
CAGGCCACCCCTTCCAAAATCCCTCTTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
GCACACCCATCTTAAGCTAAGACAGGAGGATTGTGGCTCTCCACACTAAGGCCACAGCCCATC  
CGCGTGTGTGTGCTCTTCCACCCCTGCTGGCTCTGGAGCATCCATGTCTCCAG  
GAGAGGGTCCCTAACAGTCAGCCTCACCTGTAGACACCAGGGTTCTCCGGATCTGGATGGCG  
CGCCCTCTCAGCAGCGGGCACGGTGGGGCGGGCCGGCGCAGAGCATGTGCTGGATCTGTT  
TGTGTGTCTGTGTGGTGGGGAGGGAGGGAAAGTCTTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTCTTGAGCAGGAAATAAGCTTGGCCCGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSILVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVANLLVTGKIVDHGNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKCPDNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

### **FIGURE 93**

CGGTGGCCATGACTGCGGCCGTTCGGCTGCGCCTCATTGCCCTCGGGCTGCGCTCGCC  
CTTTATGTCTCACCATGCCATCGAGCCGGTGCATCATCTTCATGCCGGAGCTTCTT  
CTGGTTGGTGTCTACTGATTGCTCCCTGTTGGTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGCTCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTTGAAGAGTATAACCC  
AGGTGAGACAGCACCCCTATGCGACTGCTGGCCTATGTTCTGGCTGGGCTTGGAATCATGA  
GTGGAGTATTTCCCTTGTGAATACCCATCTGACTCCTGGGGCAGGCACAGTGGGCATTCAT  
GGAGATTCTCCTCAATTCTCCTTATTCACTGCTGGTCATTATCTTGCTGCATGT  
ATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGAAAAAGTGGGCATCCTCCTTATCGTTC  
TCCTGACCCACCTGCTGGTGTAGCCCAGACCTTCATAAGTTCTTATTATGGAATAACCTGGCG  
TCAGCATTATAATCCTGGTGCATGGCACCTGGCATTCTAGCTGCGGGAGGCAGCTGCCG  
AAGCCTGAAACTCTGCCTGCTGCCAAGACAAGAACTTCTTACAACCAGCGCTCCAGAT  
AACCTCAGGGAACCCAGCACCTCCAAACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCT  
TTTCTGAAAATCCCTTTCTGGTGGATTGAGAAAGAAATAAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLGP GTVG IHDSPQFFLYSAFMTLVII LLHVFWGIVFFDGCEKKWGILLIVLLT  
HLLVSAQTFISSYYGINLASAFIILVLMGTWAAGGSCRSLKLCLLCQDKNFLLYNQRSR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 95**

AATTTTCACCAGAGTAAACCTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG  
GACCCAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTGTCTTAGGATCAC  
TCGGTCATTACACAGCTCAAACCTGCTTGGGACTCCCTCCCACAAAACTGGCTCCGGATCAGG  
GAACACTACCAACCAACAGCAGTCAAATCAGGTCTTCCTTAAGTCTGATACCATTAACA  
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCCTGGGAGGGTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTTGTCACACAACTGGAGCCAGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC  
TTCACGAGCCTCATCCATTCTGTTCCGGAGGCATCCTGCCACCAGTCAGGCGAGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTCCAGCAGGAGGAGCAGGTGTAATCCTGCCACCCAGG  
GAACCCCAGCAGGCCCTCCAACTCCCAGTGGCACAGATGACGACTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTTTCAAATTTCAACTAAGCTGCCTCGAATTGGTGATACTGTGAATCTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAGAAATTAACTTAAT  
TACCTGAAAATCTTGAAATTCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTAAAAA  
CAATAATTCAATGGATAAACTGTCTTGAAATATAACATTATGCTGCCTGGATGATGCAT  
TAAAACATATTGGGAAAACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM  
LTLPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTSG  
TDDDFAVTPAGIQRSTHAIIEEATTESANGIQ

Signal peptide:

amino acids 1-16

## **FIGURE 97**

GCTCAAGTGCCCTGCCTTGC~~CCC~~ACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCT  
CTTCTTGCTTGGCAGCTGGACCAAGGGAGCAGTCTTGGCGCTGGAGGGCTGTCCTGACCAATG  
GTCCCTGCCTGGCTGTGGCTTGTGTCCTCCGTCCCCCAGGCTCTCCCCAAGGCCCAGCC~~TG~~  
AGAGCTGTCTGTGGAAAGTTCCAGAAA~~ACT~~ATGGTGGAAATTCCCTTATACTGACCAAGTTGC  
CGCTGCCCGTGA~~GGGG~~CTGAAGGCCAGATCGTCTGCA~~GGGG~~ACTCAGGCCAGGAACTGAG  
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGA~~CC~~AGGCCCTGGACAGGAGA  
GCAGGCAGAGTACCCAGCTACAGGTACCC~~TG~~AGATGCAGGATGGACATGTC~~TG~~GGTAC  
AGCCTGTC~~TG~~GTGACGTGAAGGATGAGAATGACCAGGTGCCCATTTCTCAAGCATCTAC  
AGAGCTGGCTGAG~~GGGG~~TACAGGCC~~TG~~GCATCCCCCTCTCTTGA~~GG~~CTCAGACCG  
GGATGAGGCCAGGCCACAGCCAACTCGGATCTCGATTCCACATCTGAGGCCAGGCTCAGCC~~A~~  
CTTCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGCTCTGGCCCTCAGCCCCAAGGGAGC  
ACCAGCCTGACCACGCC~~TG~~AGAGGACCTACCAGCTGGTACAGGTCAGGACATGGTGA  
CCAGGCC~~TG~~AGGCCACCAGGCCACTGCCACCGTGAAGGCTCCATCATAGAGAGCACCTGGGT  
CCCTAGAGCCTATCCACCTGGAGAGAATCTAAAGTCTTACCCGACCA~~C~~ATGGCC~~A~~GGTA  
CACTGGAGTGGGGTGA~~TG~~ACTATCACCTGGAGAGCCATCCCCGGGACCC~~TT~~GA~~TG~~AA  
TGCAGAGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGGCCAGGCTGAGTACCTGCTC  
AGGTGGGGCTCAGAATTCCATGGCAGGACTATGCCGGCCCTCTGGAGCTGACGTGCTGGT  
ATGGATGAGAATGACAACGTGCC~~T~~ATCTGCCCTCCCCGTACCC~~C~~AGTCAGCATCC~~T~~GAGCT  
CAGTCCACCAGGTACTGAAGTGA~~T~~ACTAGACTGTCAGCAGAGGATGCA~~G~~ATGCCCGGCTCCCCA  
ATTCCCACGTTGTGATCAGCTCTGAGCC~~TG~~AGCCTGAGGATGGGGTAGAGGGAGAGCCTC  
CAGGTGGACCC~~TG~~AGGCCACTCAGG~~TG~~ACGCTGGGGG~~TG~~CTCCACTCGAGCAGGCCAGAACAT  
CCTGCTCTGGTGTGCC~~TG~~ACCTGGCAGGCCAGAGGGTGGCTCAGCAGCAGTGTGAAG  
TCGAAGTCGAGTCACAGA~~T~~ATCAATGATCAGGCC~~TG~~AG~~T~~TCATCACTCCAGATTGGCCT  
ATAAGCCTCCCTGAGGATGTGGAGCCGGACTCTGGTGGCC~~TG~~ACAGCCATTGATGCTGA  
CCTCGAGCCC~~TG~~CCCTCCGCC~~TG~~ACATGGATT~~TG~~CA~~TG~~AGAGGGGAGACACAGAAGGGACTTTG  
GCCTGGATTGGGAGGCCAGACTCTGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
GCAGCTCAAGTCATGAGGTGGTGGTGGCAGAGTGTGGGAAGCTGGTGGCCAGGCC  
AGGCCCTGGAGCCACGCCACGGTACTGTCCCCATCAGTGC~~CC~~CAGCCGCTCTTCTGCTGACC~~A~~  
ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGC~~CC~~CAGCCGCTCTTCTGCTGACC~~A~~  
CAGCCCTCCGACCC~~TG~~ACATCAGCCGAACCC~~TG~~CAGGTCTCCCTAGTC~~A~~ATGACTCAGAGGGCTGGCT  
CTGCATGAGAATCTCCGGGAGGTGCCACACCGCC~~TG~~CAGGGGCCAGCC~~TG~~GGGG  
ACACCTACACGGTCTGTGGAGGCCAGGATA~~C~~AGCCCTGACTCTTGCCCC~~TG~~CCCC~~TG~~CCCC  
TACCTCTGCACACCCGCCAAGACC~~TG~~GGCTGATCGTGA~~TG~~GGAGCCAGCAAGGACCC~~TG~~ATCT  
GGCCAGTGGGACGGTCC~~TG~~ACAGTCTC~~TG~~ACCTCAGG~~TG~~GGCC~~TG~~CA~~TG~~GGGAT~~TG~~GG  
GCCTCCAGACTCTCAATGGTCC~~TG~~CTGCTACCTCAGG~~TG~~GGCC~~TG~~CA~~TG~~GGGAT~~TG~~GG  
GAACACATAATCCCGTGGTGGCAGCCACATGCCAGATGTGGCAGCTCCTGGTTGAGT~~TG~~GAT  
CGTGTGCGCTGCAACGTGGAGGGCAGTGCATGCGAAGGTGGGCC~~TG~~CA~~TG~~GGGAT~~TG~~GGCC  
CGAAGCTGTGGCAGTGGCATCTTGAGGGCAGCTGGTAGCA~~TG~~AGGAATCTCCTCATCCTC  
ATTTCCACCACTGGACCATGTCAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCT  
GAAGGGACTGTCT~~TG~~ATGGCC~~TG~~AGGCAGCTAGTGGAGCTGGCCTCTGGCTCCATCTGAG  
TCCCCTGGGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGACAGAGT~~TG~~AGAAGCCCTCCA  
TCTGCCCTGGGTGGAGGCCACCATCACCATCACCA~~TG~~AGG~~TG~~GT~~TG~~GGCCAATAATAAGCC~~TG~~AGAGAA  
CTGGGCTGGGCC~~TG~~ATGGAGTGT~~TG~~CC~~TG~~AA~~TG~~TCAGGG~~TG~~TTGCC~~TG~~AA~~TG~~AA~~TG~~AA~~TG~~AG  
CTGGGCTGGGCC~~TG~~ATGGAA~~TG~~AAAA~~TG~~AAAA~~TG~~AAAA~~TG~~AAAA~~TG~~AAAA~~TG~~AG

## **FIGURE 98**

MVPAWLWLLCVSVPQALPKAQPALSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRLGALALSPKG  
STSLDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAENLKVLYPHHMAQ  
VHWSGGDVHYHLESHPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDYAAPPLEHVL  
VMDENDNVPICPPRDPHTSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVEGRA  
FQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGAEGGFSSCTCEVEVAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTEGTFLDWEPDSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLVGPGPGATATVVLVERVMPPKLDQESYEASVPISAPAGSFLLT  
IQPSDPIRTLRFSLVNDSEGWLCEIKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTTLAPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPVQRDWRLQTLNGSHAYLTLLAHWVEP  
REHIIIPVVVSHNAQMWMQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLI  
LIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## **FIGURE 99**

GGCTGACCGTGTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCACGCCCTG  
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCTGGAAAGCACCAGCCTTTA  
TCTCTTCACCTTCAGTCCCCTTCTCAAGAATCCTCTGTTCTTGCCTCTAAAGTCTTGGTAC  
ATCTAGGACCCAGGCATCTTGCTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTTATGTTGGTCTACTATTGCATTAGAAGCTGAACAAATTCAATGAGACTAGCACC  
TCTGCCAACACTGGATCCAGTGTGATCTCAGTGGAGCCAGCACGCCACCAACTCTGGTCCAG  
TGTGACCTCCAGTGGGTCAAGCACAGCCACATCTCAGGGTCCAGCGTGAACCTCCAATGGGTCA  
GCATAGTCACCAACTCTGAGTCCATACACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG  
TTCAGCAGCGTCCAGTGGGATCAGCATAGCAGCACACCCCTCAGTGGGCAAGCACAGTCACCAACT  
GGCCAGCACAGCCACCAACTCTGAGTCCAGCAGCACACCCCTCAGTGGGCAAGCACAGTCACCAACT  
CTGGGTCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC  
AGTAGGGCCAGCAGTCCACCAACTCTGAGTCTAGCACACTCTCAGTGGGCAAGCACAGCCAC  
CAACTCTGACTCCAGCACAACCTCCAGTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGCAAGCACAGCCACCAACTCTGAGTCCAGCAGCACAGCCACCAACTCTGAGTCCAG  
GCCACCAACTCTGAGTCCAGCACAACCTCCAGTGGGCAAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCAATGGGCTGGCACAGCCACCAACTCTGAGTCCAGCAGCACAGCCACCTCCAGTGGGCA  
GCACAGCCACCAACTCTGACTCCAGCAGCACAGTGTCCAGTGGGCAAGCACAGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGCAAGCACAGCCACCAACTCTGAGTCCAGCACAGCCACCTCCAGTGG  
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACCTCCAGTGGGCGGGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCC  
AGTGGGCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCAACACAGCCAC  
CAACTCTGAGTCCAGCAGCACAGTGTCCAGTGGGCAAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACCTCCAGTGGGCTAGCACA  
GCCACCAACTCTGACTCCAGCACAACCTCCAGTGGGCAAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAGCCACCAACTCTGAGTCCAG  
ACACAGCCACCAACTCTGGGTCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA  
ATGCACACAACCTCCATAGTCATCTACTGAGTGTGAGGCAAAGCCTGGTGGGTCCCTGGT  
GCCGTGGAAATCTCCTCATACCCCTGGCTCGGTTGCGGGCGTGGGGCTCTTGTGGC  
TCTTCTCTGTGTGAGAAACAGCCTGTCCTGAGAAACACCTTTAACACAGCTGTCTACCACCCCT  
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAAATCATGGAGCCCCACAGGCCCAG  
GTGGAGTCCTAACTGGTCTGGAGGAAGCAGTACATCGATAGCCATGGAGATGAGGGAGGA  
ACAGCGGGCCCTGAGCAGCCCCGGAAAGCAAGTGCCTGAGGAAAGGAAGAGACCTGGCA  
CCCAAGACCTGGTTCTTCATTCATCCCAGGAGACCCCTCCAGCTTGTGAGATCTGAA  
AATCTTGAAGAAGGTATTCTCACCTTCTGCTTACAGACACTGGAAAGAGAAACTATAT  
TGCTCATTAGCTAAGAATAATACATCTCATCTAACACACAGACAAAGAGAAGCTGTGCTTG  
CCCCGGGGTGGGTATCTAGCTGAGATGAACCTCAGTTAGGAGAAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKM**Q**GNVLLM**F**LLL**H**EAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSG**I**ATNSESSTTSSGASTATNSESSTPSS  
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
STTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGLVPWEIFLITLVSVVA  
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP~~PG~~GNHGAPHRPRWSPNWFWR~~RP~~VSSI  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

## **FIGURE 101**

GGCCGGACGCCTCCCGTТАCGGGATGAATTAACGGCGGGTCCGCACGGAGGTGTGACCCCTA  
CGGAGCCCCAGCTTГCCCACGCACCCCACTCGCGTГCGCGCGTГCCCTGCTTGTACAGGTG  
GGAGGCTГGAACTATCAGGCTГAAAAACAGAGTGGTACTCTCTГGGAGCTГGCAACAAAT  
GGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTГCTCTGAACCCATGGTCAATT  
AACGAGGCAGTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAGCTTГGAATCAT  
GGTGTCACTГGAAAGGGATTACTTTACTGTACTCTГTTGGGAGCTTTTГGAAGCATTT  
TCATGCTGAGTCCCTTTACCTTGATGTTГTAAACCCATCTГGTATCGCTГGATCAACAAAC  
CGCCTTГGGCAACATGGCTCACCTACCTГGGCATTATTGGAGACCATGTTГGTГAAAGT  
GATTATAACTGGGATGCATTГTCCТГGAGAAAGAAGTGTCAATTATCATGAACCATCGGACAA  
GAATGGACTGGATГTCCТГGАATTГCCTGATGCGATATAGCTACCTCAGATTГGAGAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTГTCCТГGАATTГGTTГGGCAGTGCAGGCTГCCTATAT  
CTTCATTCA TAGGAAATГGAGGATGACAAGAGCCATTГGAAGACATGATTGATTACTTTГTГ  
ATATTCACTGАACCACTCAACTCCTCATATTCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTГCTГAAAAAAATGGACTTCAGAAATATGAATATGTTACATCCAAG  
AACTACAGGCTTACTTTГGGTAGACCGTCAAGAGAAGGTAAGAACCTTГATGCTГTCCATG  
ATATCACTGTГGCATCCTCACAAACATTCTCAATCAGAGAAGCACCTCCTCAAGGAGACTTT  
CCCAGGGAAATCCACTTCACGTCCACCGGTATCCAATAGACACCCCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTГГTГCCACAAACGGTГGGAGAGAAAAGAGAGAGGCTГGTTCCATCAAG  
GGGAGAAGAATTTTATTACCGGACAGAGTGTCAATTCCACCTГCAAGTCTGAACTCAGGGTC  
CTTГГTГCAATTГCTCTATACTGTATTГGACCCCTГTГCAGCCCTГCAATGTГCCTACTCAT  
ATATTГTACAGTCTГTTAAGTГGTATTATACCACTGTAAATCTTГTГCTГCAAGAGA  
GAATATTГGTГGAGACTGGAGATCATAGAAACTГCATГTTACCGACTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAATGAGTAAGATTAAAGTTГCCATGTGAAAACCTAGAGCATATTГTГ  
GAAATГTCTAAACCTTCTAAAGATATTГCACTTAATTГTГGGAAAATATTГCTACAATT  
GCCATCATTATTГTTAAAGATATTГCACTTAATTГTГGGAAAATATTГCTACAATT  
TTAATCTCTГAATGTAAATTГGАACTGTГTACATAGCAGGGAGTГATGГGGTГAAATAACTT  
GGCCAGAATATTAAACAATCATCAGGCTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFGIMVSWKGIYFILTLFWGSFFGSIFMLSP  
FLPLMFVNPSWYRWINNRLVATWLTPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCLMRYSYLRLEKICLKASLKGVPGFWAMQAAAYIFIHRWKDDKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSRSNAEAKNGLQKYEYVLHPRTGFTFVVDRLREGKNLDAVHDITVA  
YPHNIPOSEKHLLOQDFPREIHFHVRYPIDTLPTSKEDLQLWCHKRWEEKERLRSFYQGEKNF  
YFTGQSIPPKCKSELRLVVKLLSILYWTLFSPAMCLLILYSLVKWYFIITIVFVLQERIFGG  
LEIIELACYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

### **FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCACGGCTCTGCGCTGAGACAGCTGGCCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTCTAGTGTAGATCAACCCACAGGAATA  
TCCATGGCTTTGTGCTCATTGGTTCTCAGTTCTACGAGCTGGTGTAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTGTCCAGGGCTTGGTGGGGGAGGACGCCGTGTTCTCTGCTCCCTCT  
TTCCCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAGTTCCATGCTGTGGTC  
CACCTCTACAGAGATGGGAAGACTGGGAATCTAACAGATGCCACAGTATCGAGGGAGAACTGA  
GTTTGTAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGCTAAAAAACATCACTCCCTCGG  
ACATCGGCCTGATGGGTCTGGTTCACTGTTCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGGCAGCACTGGGCTCACTCCCTCATTTCCATGTTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCCCTGAGCTGGGTTCCAGGCTGGGATCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
AGGATTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGGAAATCCAAGGTATTGATAGGAGAGACGTTTCCAGGCCCTCACCTGGCCCTGGCTTCTA  
TTTACTCGGGTTACTCTGTGGCTGTGGTGTGTCATGGGATGATAATTGTTCTTC  
AAATCCAAAGGAAAATCCAGGCGAACACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG  
AGACGCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCTGCG  
TTTCTGATCTGAAAATCTGTAACCCATAGAAAAGCTCCCCAGGGAGGTGCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAATGTAGGGTGGTATGTGGAGTGTGTCGGGATGACGTAGACAGGGGAAGAACAA  
ATGTGACTTGTCTCCAAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTC  
ACATTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCTACAGGAGTAGGGGTCTTCC  
GGACTATGAGGGTGGGACCATCTCTTCAATACAAATGACCAGTCCCTTATTATACCCCTGC  
TGACATGTCAGTTGAAGGCTTGTGAGACCCATATCCAGCATGCGATGTATGACGAGGAAAAG  
GGGACTCCCATATTCAATGTCAGTGTCTGGGGTGAGACAGAGAACCCCTGCTAAAGGGC  
CCCACACCACAGACCCAGACACAGCCAAGGGAGGTGCTCCGACAGGTGGCCCTAGCTTCC  
CCGGAGGCTGCGCACAGAGAGTCAGCCCCACTCTCTTAGGGAGCTGAGGTTCTCTGCC  
TGAGCCCTGAGCAGCGGAGTCAGCTCCAGATGAGGGGGATTGGCCTGACCCGTGGAG  
TCAGAAGCCATGGCTGCCCTGAAGTGGGAGGAATAGACTCACATTAGGTTAGTTGTGAAAAA  
CTCCATCCAGCTAACGATCTGAACAAGTCACAACCTCCAGGCTCCTCAATTGCTAGTCACGG  
ACAGTGATTCTGCCTCACAGGTGAAGATTAAAGAGAACAGAATGTGAATCATGCTTGAGGTT  
TGAGGGACAGTGTGCTAATGATGTGTTTATATTACATTCCCACCAAAACTCTGTT  
TGCTTATTCCACATTAATTACTTTCTCTATACAAATCACCCATGGAATAGTTATTGAACACC  
TGCTTGTGAGGCTAAAGAATAAAAGAGGGAGTAGGATTTCACTGATTCTATAAGCCCAGCAT  
TACCTGATACCAAAACAGGCAAGAAAACAGAAGAAGAGGAAGGAAAACACAGGTCCATATCC  
CTCATTAAACACAGACACAAAAATTCTAAATAAAATTAAACAATAAACTAAACAATATAATTAA  
AAGATGATATATAACTACTCAGTGTGGTTGTCCCACAAATGCGAGGTTGTTAATATTAAAT  
ATCAACCAGTGAATTCACTGAGCACATTAATAAAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCSSGWFPQPTAKWKGPOQGDLSSDSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPSPWRLASILLGLLCGALCGVVMGMIIVFFK  
SKGKIQAEQELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSNNNGYWVRLTTEHLYFT  
FNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPIQHAMYDEEKG  
TPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## **FIGURE 105**

CCTTCACAGGACTCTCATTGCTGGTGGCAATGATGTATCGGCCAGATGTGGTAGGGCTAGGAAAAGAG  
TTTGGTGGAAACCTGGTATCGGCCGTCATCTTCATATCCCTGATTGCTGGCAGTGTGCATTGGA  
CTCACTGTCATTATGTGAGATATAATCAAAGAACGCTACAATTACTATAGCACATTGTCATTACAAC  
TGACAAACTATATGCTGAGTTGGCAGAGAGGCTCTAACAAATTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTGGAAAATGCATTTATAATCTCCATTAAGGGAAAGAATTGTCAGTCTCAGGTTATCAAGTTC  
AGTCAACAGAACGATGGAGTGTGGCTCATATGCTGTTGATTGAGATTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTGTTCAACTTGTACATGAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
ATCCTCACTCAGTAAAATTAAAAAAATCAACAAGAACAGAACAGACAGCTATCTAAACCATGCTGCCGA  
ACACGAAGAAGTAAAACCTCTAGGTAGAGTCTCAGGATCGTGGTGGACAGAAGTAGAAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCACCTTAATTAGCCACATGGC  
TTGTGAGTGTGCTCACTGTTACAACATATAAGAACCTGCCAGATGGACTGCTTCCTTGGAGTAACA  
ATAAAACCTTCGAAAATGAAACGGGTCTCCGAGAAATAATTGTCATGAAAATACAAACACCCATCACA  
TGACTATGATATTCTCTTGAGAGCTTCTAGCCCTGTTACACAAATGCACTACATAGAGTTGTC  
TCCCTGATGCACTCATGAGTTCAACCAGGTAGTGTGATGTTGTGACAGGATTGGAGCACTGAAAC  
GATGGTTACAGTCAAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAACATTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTAGAAGGAAAACAGATGCAT  
GCCAGGGTGACTIONGGGACCCTGGTAGTCAGATGCTAGAGATATGGTACCTTGCTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTTACTAGAGTTACGGCCTTGCGGGACTG  
GATTACTTCAAAACTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTGTTTGTGTTTG  
GGTGTGGAGGCCATTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCA  
ATAAAACTGTTGCTTGTGATGCACTGTTCTAGAAGTTGTCAGAATTGACTGTTGACATAATTGTAAT  
GATCAACTCTGTCATCTGTGAGCAATGAACTTTATGTACATAGAGAAATAGATAATACAATTAC  
ATTACAGCCTGTATTCACTTGTCTAGAAGTTGTCAGAATTGACTGTTGACATAATTGTAAT  
GCATATATAACAATTGAAGCACTCCTTCTTCAGTCTCAGCTCCTCTCATTTCAAGAAATATCCATT  
TCAAGGTGCAGAACAGGAGTGAAAGAAAATAAGAAGAAAAATCCCTACATTATTGGCACAGAA  
AAGTATTAGGTGTTCTTAGTGGAAATTAGAAATGATCATATTCAATTGAAAGGTCAAGCAAAGACA  
GCAGAACATCAACTTCATCAATTAGAAGTATGGAAACTAAGTTAAGGAAGTCCAGAAAGAACCAAG  
ATATATCCTTATTTCATTCACAAACTACTATGATAATGTGAAGAAGATTGTTGACCT  
ATAATAATTATAACAAACTTCATGCAATGTAATTGTCAGCAAATTAAAGCAAATTATTAACATTG  
TTACTGAGGATGTCAACATATAACAAATAAAATATAACACCCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTGHYVRYNQKKTYNYYSTLSFTTDKLY  
AEFGREASNNFTEMSRQLESQMVNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
RRIIVHEKYKHPHDYDISLAELOSSPVPTNAVRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTNCNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIWYLAG  
IVSWGDECAPNPKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## **FIGURE 107**

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCCCTCGGCTCTCCGCGAAGAAAGTCCCTG  
CCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCCAGC  
GCCGACGATCGCTGCCGTTTGCCTTGGGAGTAGGATGTGGTGAAGAGATGGGCTTCTCCCT  
ACGGGGCTCACA**AT**GGCCAGAGAAAGATTCCGTGAAGTGTCTGCGCTGCTACGCCCTCAA  
TCTGCTTGGTTAATGTCCATCAGTGTGTTGGCAGTTCTGCTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTGACTTCTCCT  
GTGGTTCATCGGTATGGCTGTTGCTGTTCCCTATCATTGTTGGGATGTTAGGATATTG  
TGGAACGGTGAAGAAAGATCTGGCTTGGACATGAGAACAGGAACCTATGGTCCAGTACAATGGTCA  
GATATGGTCACTTGAAGGCCAGGATGACAATTATGGATTACCTAGATATCGGTGGCTTACTCA  
TGCTTGAATTTCAGAGAGGTTAAGTGTGGAGTAGTATTTCACTGACTGGTGG  
AAATGACAGAGATGGACTGGCCCCAGATTCTGCTGTGTTAGAGAATTCCAGGATGTTCCAAA  
CAGGCCACCAGGAAGATCTCAGTGACCTTATCAAGAGGGTGTGGGAAGAAATGATTCCCT  
TTTGAGAGGAACCAACAACGAGGTGCTGAGGTTCTGGGAATCTCCATTGGGTGACACAAA  
TCCTGGCATGATTCACCATTACTCTGCTCTGGGCTCTGATTATGATAGAAGGGAGCCGG  
ACAGACCAAATGATGTCTGAAGAATGACAACACTCTCAGCACCTGTATGTCCTCAGTAGAACT  
GTTGAAACCAAGCCTGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAAACACACT  
TTGAGATGGAGGAGTT**TAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGT**TTTATTGGACT  
TGTGAATTGGAGTACATACTATGTGTTAGAAATATGTAGAAATAAAATGTTGCCATAAAA  
TAACACCTAAGCATATACTATTCTATGCTTAAATGAGGGATGAAAGTTCAATGTCTAAGTC  
ACCACCTGGACAATAATTGATGCCCTAAATGCTGAAGACAGATGTCATACCACTGTGTAGCC  
TGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATTTCCGCA  
TCCATGCAAACGAGTCACATATGGGGACTGGAGCCATAGTAAAGGGTGAATTACTTCTACCAA  
CTAGTATATAAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA  
CTCAGCGATCTATTCTCTGATGCTAAATAATTATATACAGAAAACCTTCATAATTGGTACT  
ACCTAAATGTGATTGGTCTGGTTACTAAATATTCTTACCACTTAAAGAGCAAGCTAACACAT  
TGTCTTAAGCTGATCAGGGATTGGTATATAAGTCTGTAAATCTGTATAATTCACTGCGAT  
TTCAGTTCTGATAATGTTAGAATAACCATATGAAAAGGAAATTGTCCTGTATAGCATCATT  
ATTGGTACTTCTGCTGTTAATAAGCTTACTATTCTGCTCTGGGCTTATATTACACATATAAC  
TGTATTTAAATACCTAACCAACTAATTGGAAAATTACCACTGTGATACATAGGAATCATTATC  
AGAATGTAGTGTGCTTTAGGAAGTTAAATAAGAAAATTGCACTAACACTTAGTTGATTGAGA  
AAGGACTTGTATGCTGTTTCTCCAAACAGAAGACTCTTTGACACTAAACACTTTTAAAGA  
GCTTATCTTGCCTCTCCAAACAGAAGCAATAGTCTCAAGTCAATATAAAATTCTACAGAAA  
TAGTGTCTTTCTCCAGAAAATGCTTGAGAATCTTAAACATGTGACAATTAGGATT  
CTTGTGTTATTCACTGATTAAATACTGTGGCAAATTACACAGATTATTAATTTTTACAA  
GAGTATAGTATATTATTGAAATGGAAAAGTCATTACTGTATTGTGTTGTTAT  
TTCTCAGAATATGAAAGAAAATTAAATGTCATAAAATTTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNVLTLAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLOQVLRLFLGISIGVTQILAMILTITLLWALYYDRREPQTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## **FIGURE 109**

CCAAGGCCAGAGCTGGACACCTTATCCCACATCCTCATCCTCTTCTCTGATAAAGCCCCTACCAGTGCT  
GATAAAAGCTTTCTCGAGAGCCTAGAGGCCCTAAAAAAAGTGCTTGAAGAGAAGGGGACAAAGGAACA  
CCAGTATTAAGAGGATTTCCAGTGTTCCTGGCAGTTGGTCCAGAAGGATGCCTCCATTCTGCTTCTCACCTG  
CCTCTTCAACAGGCACCTCCGTGTCACCCGTGCCCTAGATCCTTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCAGTGGATGAGTCAGGTCTCAAGGCTCCCTATGTGACAACCATGTGAATGGGAG  
TGGTACCACTTCACGGGCATGGCGGGAGATGCCATGCCCTACCTCTGCATACAGAAAACCAGTGGAAACCCA  
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCAGGGCATTGTGCAACGCCAGGCTGTGCCAGCT  
TCAATGGGAACACTGTCTCTGGAACACACCACGGTGGAAAGTCAGGCTGCCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCAATTGATGACATCTGCGACGAGGACTGCCATGG  
CAGCTGCTCAGATACCAGCGACTGCACATGCCCTCAGGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTG  
ATGAAAATGAATGTGAGCAAACACGGTGGCTGAGTGTGAAACCTCAAAACTCTACCGCTGT  
GAGTGTGGGTTGGCGTGTGCTAAGAAGTGTGCAAGACTGTGAAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTTGCCTGGATCTGAGAAAGGCTACAGTGTGAAATGTCCCAGGGCTGGTGTG  
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAATCAAATGCCATGAAAGTGAACATCCCCAGGGAG  
CTGGTTGGTGGCTGGAGCTTCTGACCAACACCTCTGCCAGGAGTGTCCAACGGCACCCATGTCAACAT  
CCTCTCTCTCAAGACATGTGGTACAGTGGTCAAGTGTGAAATGACAAGATTGTGGCCAGCACCTCGTGA  
CAGGTCTACCCAAGCAGACCCGGGGAGCAGCGGGACTTCATCATCCGAACCAAGCAAGTGTGATCCCCGGT  
ACCTGCGAGTTCCACGCCTGTACACCATTCTGAAAGGATACGTTCCAAACCTTCGAAACTCCCCACTGGAAAT  
CATGAGCCGAAATCATGGATCTTCCATTCACTCTGGAGATCTCAAGGAAATGAGTTGAAGAGCCTTAC  
GGGAAGCTCTGCCACCCCTCAAGCTCGTCACTCCCTACTTGGCATTGAGCCCGTGGTGCACGTGAGCGG  
TTGGAAAGCTTGGTGGAGAGCTGCTTGCACCCACCTCCAAAGATCAGCAGGGACTCTGAAATACTACCTCAT  
CCGGGATGGCTGTGTTCAAGATGACTCGGTAAGCAGTACACATCCGGGATCACCTAGCAAAGCACTTCCAGG  
TCCCTGTCTCAAGTTGTGGCAAAGACCACAAGGAAGTGTGACTGCCGGTTCTGTGTGGAGTG  
TTGGACCGCGTCCCGCTGTGCCACGGCGATCCGCATCGACTGGAGGACTTAGTTCGTAGCCATACCTC  
CGGTCTACAGGGCCAGACGCTAACAGCGGCCGATCCGCATCGACTGGAGGACTTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTGGAGCTCTCCCCCACCAGGCTCTAAAGAACATCTGCCAACAGC  
TGGGTTCAAGACTTCAACTGTGAGTCAGACTCCAGCACCACACTCACTGATTCTGGTCATTCACTGG  
CAGGTACAGCAGCTGAACAATGTGGCCTGGTGGGTTCATCTTCTAGGGTTGAAAACACTAAACTGTCCA  
CCCAGAAAGACACTCACCCATTCCCTCATTTCTTCAACTTAAACACTCGTGTATGGTGAATCAGAC  
CACAAAATCAGAAGCTGGTATAATATTCAGTACAAACCTAGAAAAAATAAACAGTTACTGAAATTATGA  
CTTAAATACCAATGACTCCTAAATATGTAATTAGTTACCTTGAAATTCAATTCAAATGCAGACTAA  
TTATAGGAAATTGGAAGTGTATCAATAAACAGTATATAATT

## **FIGURE 110**

MPPFLLITCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPEHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNNTTVEVKACPGGYYVRLTKPSVCFHV  
YCGHFYDICDEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSDGKTCEDVEGCHNNNGCShSCLGSEKGYQCECPRLVLSEDNHTCQVPVLCKSNAIEVNIPRELVGG  
LELFILTNTSCRGVSNGTHVNILFSLKTCGTVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPPFTLEIFKDNEFEEPYREALPTLKLRLDSLYFGIEPVVHV  
SGLESLVEESCFTPTSKIDEVLKYLLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
LVCGVLDERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## **FIGURE 111**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCCCTGCACCTGG  
GCCTCCTCCAGCCAGTGCTGACCAAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGAGGCCCT  
CCTGCTGCCCTGGGGTGAACATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCGTATCCCC  
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT  
GGTTGCTCTCATCAAGGTGATTCTGGATAAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC  
CCCGAAGGGCCTGCAGTGGCAGTCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC  
AGGGAACCTGGTCTCTGCCTGTTGACAACTTCACAGAAGCTCTCGTGGACAGCAGCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGGCCAGACCAAGGATCTGGATGTTGAAATCACAGAAAACAGCCAG  
GAGCTTCGCATGCGGAACATCAAGTGGCCCTGTCAGGCTCCCTGGCTCCCTGCACGTCTGGCCTG  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGGAGGAGGAGCCTGTGGATTCTGGCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGGAGGGAGCATTCTGGACCCCCACTGGTCCCTCACGGCA  
GCCCACTGCTTCAGGAAACATACCGATGTGTTCACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGCAG  
CTTCCCACCTCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTCCCACACTCACTTCAGGCACAGTCAGGCCATCTGCTGCCCTTCTT  
GATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATGGATGGGCTTACGAAGCAGAATGGAGGGAA  
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGT  
ACCAGGGGAAGTCACCGAGAAGATGATGTGTCAGGCATCCCGAAGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGGCCCTGTGATGACCAATCTGACCAAGTGGCATGTGGTGGCATCGTTAGCTGGCTATGG  
CTGGGGGGGGCCGAGCACCCAGGAGTATACACCAAGGTCTAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTGTAATGCTGCTGCCCTTGCAGTGTGGAGGCCCTCCTGCCCTGCCACCT  
GGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCTGGTACACCCCTCTGCCACAGCCTCAGCAT  
TTCTGGAGCAGCAAAGGGCCTCAATTCTGTAAGAGACCCCTCGCAGGCCAGAGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTGGCCACACTTGGTGTCCCAGCATCCAGGGAGAGACACAGCCCACGTAAACAGGTCT  
CAGGGGTATTGCTAAGCCAAGGAACCTTCCCACACTACTGAATGAAAGCAGGCTGTCTGTAAAGCC  
CAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGGCCCTGTCCGTCTCACCCATCCCCAA  
GCCTACTAGAGCAAGAAACCAAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTCATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTGTAACATCTGGCAAAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIP III ALLSLASIIIVVVLIKVILDKYFLCG  
QPLHFI PRKQLCDGELDCPLGEDEEHCVKS FPEGPAVAVRLSKDRSTLQVLD SATGNWFSACFDN  
FTEALAE TACRQMGYSRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSLHCLACGKSL  
KTPR VVGEEASVDSWPWQVSIQYDKQHVC CGSILD PHWVL TAAHCFRKHTDVF NWKVRAGSDKL  
GSFPSLAVAK III IFNPMYPKDNDIALMKLQFPLTFSGTVRPICL PFFDEELTPATPLWIIIGWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDT CQGDGGPLMYQS  
DQWHVVGIVSWG YGC GGPSTPGVYTKV SAYLNWI YNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (type II)

## **FIGURE 113**

GGCTGGACTGGAACCTCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTCACTGCAACTAAAAAGCCACAGGGAGT  
TGAACTGCTAGGATTCTGACTATGCTGTGGCTAGTGCTCCTACTCCTACCTACATTAAAATC  
TGTTTTTGTTCTCTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCACACCGTCCCCTGAAG  
CCGGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCTCACCAACTGTCTACGTCT  
GGAGGCAGTCACTCGGGCAGTCAGGTAGCTGAGCCTCTGGTAGCTGCGGCTTCAAGGTGGC  
CTTGCCCTGGCGTAGAAGGGATTTGACAAGCCCAGAAGATTCATAGGCATGGCTCCACTGCC  
AGGCATCAGCCTGCTGTAGTCAACTACTGCCCTGGGCCAGGACGGCCGTGGACACCTGCTCA  
GAAGCAGTGGGTGAGACATCACCGCTGCCGCCATCTAACCTTCTATGTCCTGCACATCACCTG  
ATCCATGGGCTAACATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGTCTGCTTAGACCACCTGGTTATGTGACAGGACTTGCAATTCTCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAGGAACCTTGTGCCAATTATGGGTAGAAAAGATG  
GAGGTGTTGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGGACATGTGGGGAAAGGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGAT  
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCATGCTCTCATCAGCCAGGCAGCCAAAA  
TCTGCGATCACCAGCCAGGGCAGCCGTGGAGGCAAGCAAAGTGACCAATTCTCTCTCC  
CTCCTCCCTCTGAGAGGCCCTCTATGTCCCTACTAAAGCCACCGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGGTGGCCAGGAGGTCAAGCACAGGCTGCAAGGCTGAGAGCTGATCAGAAGGGCTGCT  
GTGCGAACACGAAATGCCCTCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG  
CTCAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTT  
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTGTGATTTGAAATTGAAACCCCCAAATCCA  
AACCTAAGAACCAAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTGGCTGTAATGCCAACAT  
TTTGGGAGGCCAGGGCGGGTAGATCACCTGAGGTCAAGGACAGCCTGGCCAACATGG  
TGAAACCCCTGTCTACTAAAAAATACAAAAAAACTAGCCAGGCATGGTGGTGTGCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAACACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAGAATTA  
TGGTTATTTGTAA

## **FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLTRAVQVAEPLGSCGFQGGPCPGRRD

**Signal peptide:**

amino acids 1-15

## **FIGURE 115**

CAGCAGTGGTCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTAAATCCAAGAAA  
ATATGTAATCACTTAAGATTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAATTGTCT  
GTTTGGGGGAGCAAGCACTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGATTACATGGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTAAAACGGATAACACTGG  
CATCTACTCGTGGTCTCAAAAATGTTTATCAAAACTCAGATTAAGTGATTCTGAATT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCAACTTTCTTGAAACAGTCAGT  
ATTTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTCTTAAAATTCCAAAATTCTGGA  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACCTAATATCAGTTCTGAGTTACAAG  
ACTTTGAGGAGGGAGGAGAAGATCTTCACTTCCCTGCCAACGAAAAAAAAGGGATTGAACAAAAT  
GAACAGTGGTGGTCCCTCAAGTGAAGTAGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGA  
AGAACTCCAATAAATGACTATACTGAAAATGGAATAGAATTGATCCCACGCTGGATGAGAG  
GTTATTGTTGATTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCTGTGAACCTTACTA  
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGCGTGTACATGCCCTG  
TAACTGGTGGTGGCCCGATGCTGGGGAGGGCTTAATAGGAGGTTGAGCTAAATGCTTAAAC  
TGCTGGCAACATATAAAATGCATGCTATTCAATGAATTCTGCCATGAGGCATCTGGCCCT  
GGTAGCCAGCTCTCCAGAATTACTGTAGGTAATTCCCTCTTCATGTTCTAATAAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAYDME  
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEIITTFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPAEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYENGIEFDPMED  
ERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

## **FIGURE 117**

GAGCTCCCTCAGGAGCGCGTTAGCTTCACACCTCGCAGCAGGAGGGCGGCAGCTTCTCGCAGGGCA  
GGCGGGCGGCCAGGATCATGTCCACCACATGCCAAGTGGTGGCGTCCCTGTCATCCTGGGCT  
GGCGGCTGCATCGGGCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT  
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCC  
TATTCACCATCCTGGACTTCCAGCCATGCTCGAGGAGCTGCGAGCCCTGATGATCGTAGGCATCGCCT  
GGGTGCCATTGGCCTCTGGTATCCATCTTGCCTGAAATGCATCCGATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTCATTGTCTCAGGTCTTGCAATTGCTGGAGTG  
TCTGTGTTGCCAACATGCTGGTACTAACTTGGATGTCCACAGCTAACATGTACACCGCATGGTGG  
GATGGTGCAGACTGTCAGACCAGGTACACATTGGTGCCTGCTGGCTGGCTGGTCGCTGGAGGCC  
TCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGCCTGGCACCAGAAGAAACCAACTACAAA  
GCCGTTCTTATCATGCCCTCAGGCCACAGTGGCTACAAGCCTGGAGGCTCAAGGCCAGCAGTGGCTT  
TGGGTCCAACACCAAAAAACAAGAAGATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTATC  
CTTCCAAGCAGACTATGTGTAATGCTCTAACACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTCA  
CCCCAAAACAAGGAGATCCCATCTAGATTCTCTGCTTTGACTCACAGCTGGAAGTTAGAAAGCCT  
CGATTTCATCTTGGAGAGGCCAATGGTCTTAGCCTCAGTCTGTCATAAATATTCCACCATAAAACA  
GCTGAGTTATTATGAATTAGAGGCTAGCTCACATTCAATCCTCTATTCTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGGTTAATCTCTCTCACATTGATGATTTAGACAGACTCCCCCTC  
TTCCCTCTAGTCATAAAACCCATTGATGATCTATTCCCAGCTTACCCCCAGAAAACCTTTGAAAGGAAA  
GAGTAGACCCAAAGATGTTATTCTGCTGTTGAATTGCTCCCCACCCCAACTGGCTAGTAATAA  
ACACTTACTGAAGAAGCAATAAGAGAAGATTTGTAATCTCTCCAGCCCAGTCTCGGTTTCTT  
ACACTGTGATCTAAAGTTACCAACCAAAAGTCATTTCACTGGTGGAGGCAACCAACCTTCTACTGCTG  
TTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCCACTGGAGTCCCTTTCTGT  
CGCGGGTCAGAAATTGTCCTAGATGAATGAGAAAATTATTTTTTAATTAAAGTCCTAAATATAGTTAA  
ATAAAATAATGTTAGAAAATGATACTATCTCTGTAATAGCTCACCCTACATGTGGATAGAAG  
GAAATGAAAAAATAATTGCTTGACATTGCTATATGGTACCTTGAAAGTCATGCTTAAGTACAAATTCC  
ATGAAAAGCTCACACTGTAATCTAGCAGTTGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAGT  
TCGAGACTAGCCTGGCAACATGGAGAAGCCCTGCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA  
TGGTGGCATACACCTGTAGTCCCAGCATTCCGGAGGCTGAGGTGGAGGATCACTTGAGCCAGGGAGGT  
TGGGGCTGAGTGAACCCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAA  
AATAAAAATAATGAAACACAGCAAGTCCTAGGAAGTAGGTTAAAACATAATTCTTTAA

## **FIGURE 118**

MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYP SKHDY  
V

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## **FIGURE 119**

GGAAAAACTGTTCTCTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTTCCGGAGTCC  
AGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCTAGAAATCGCTGGCTGTTCTTGTG  
GTGGTGGATGGGGCACAGTGGCTGTCAGTGTCTGCCTCAGTGGAGAGTGTGGCCTTCATT  
GAAAACAACATCGTGGTTTGTGAAACTCTGGAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTCAAATCTATGATTCCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG  
GACTGATGTGCTCCGTGATGTCCTCTGGCTTCATGATGCCATCCTGGCATGAAATGC  
ACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGTCAGGGCTGGAATCATCTTCAT  
CATCACGGCATGGGGCTCATCCCTGTGAGCTGGGTGCAATGCCATCATCAGAGATTTCTATA  
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCA  
CTGGTGCCTGATTGTTGGAGGAGCTCTGTTCTGCGTTTTGTTGCAACGAAAAGAGCAGTAGCTA  
CAGATACTCGATACCTCCATCGCACAACCAAAAAAGTTATCACACCGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTGTAGTTGTATGTTTAACTTAACTAAAGCCATGCAAATG  
ACAAAAATCTATATTACTTCTCAAATGGACCCCAAAGAAACTTGTATTACTGTTCTTAACGCCT  
AATCTTAATTACAGGAACGTGCATCAGCTATTGATTCTATAAGCTATTGCAGCAGAATGAGATA  
TTAAACCAATGCTTGATTGTTAGAAAGTATAGTAATTGTTCTAAGGTGGTCAAGCCTA  
CTCTTTTATCATTACTTCAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGTAAACATTATCTCACATAGAGACATGCTTATATGGT  
TTTATTAAATGAAATGCCAGTCCATTACACTGAATAAAATAGAAACTCAACTATTGCTTCTCAGGGAA  
ATCATGGATAGGGTGAAGAAGGTTACTATTAAATTGTTAAAAACAGCTAGGGATAATGCTTCCA  
TTTATAATGAAGATTAAATGAAGGCTTAACTCAGCATTGTAAGGAAATTGAATGGCTTCTGATAT  
GCTGTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTATCCTCTCAGGGCTTTTT  
CTTGTGATTAAATTAAACATTAAACGCAAGATATTGTCAGGGCTTGCATTCAAACGTCTT  
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTGGTTAGGAAAGTG  
AAAATTTTGTGTTGTATTGAAGAAGAATGATGCATTGACAAGAAATCATATATGTATGGAT  
ATATTAAATAAGTATTGAGTACAGACTTGGAGGTTCATCAATATAAAAGAGCAGAAAAATA  
TGTCTGGTTTCTTGTGTTACCAAAAAACACAACAAAAAAAGTGTCTTGTGAGAAACTCACCT  
GCTCCTATGTGGGTACCTGAGTCAAAATTGTCAATTGTTCTGTGAAAATAAATTCTCTGTA  
CCATTCTGTTAGTTACTAAATCTGAAATACTGTATTGTTCTGTGTTATTCAAATTGATGAA  
ACTGACAATCCAATTGAAAGTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT  
TATACATTATATTAAATAATTGTACATTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSIFIENNIVFENFWEGLWMNCVRQANIRMQCK  
IYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG  
MVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTALVLIVGGALFCCVFCCNEKSSY  
RYSIPSHRTTQKSYHTGKKSPSVYRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## **FIGURE 121**

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGGAG  
CCAGACGCTGACCACGTTCCCTCCTCGGTCTCCCTCCGCCCTCCAGCTCCCGCTGCCCGCAGCC  
GGGAGCCATGCGACCCCAGGGCCCCGCCGCCCTCCCGCAGCGGCTCCGCGGCCCTGCTGCTCC  
TGCTGCTGCAGCTGCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG  
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGGCCAATGTATTCCGGTACACCTGGATCCAGGTGGGATG  
GATTCAAAGGAGAAAAGGGGAATGTCGAGGGAAAGCTTGAGGGACTCTGGACACCCAAC  
AAGCAGTGTTCATGGAGTTCAATTGAATTATGGCATAGATCTGGAAAATTGCGGAGTGTA  
CATTACAAAGATGCGTCAAATAGTGTCTAAGAGTTGTTCACTGGCTCACTTCGGCTAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTTCACATTCAATGGAGCTGAATGTCAGGACCTCTCC  
ATTGAAGCTATAATTATTGGACCAAGGAAGGCCCTGAAATGAATTCAACAATTAAATT  
CATCGCACTTCTGTGGAAGGACTTGTGAAGGAATTGGTGGATTAGTGGATGTTGCTATCTGG  
TTGGCAGTTGTCAGATTACCCAAAAGGAGATGCTTCACTGGATGGAATTGAGTTCTCGC  
ATTATTGAAGAACTACCAAAATAATGCTTAATTTCAATTGCTACCTCTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTAAATAAGTTATGTATAACATCTGAATGAAAAGCAA  
CTAAATATGTTACAGACCAAAGTGTGATTACACTGTTAAATCTAGCATTATTCA  
TTCAATCAAAAGTGGTTCAATATTTTTAGTTGGTTAGAATACTTCTTCAGTCACATT  
CTCTCAACCTATAATTGGAATATTGTTGGTCTTTGTTCTTAGTATAGCATT  
AAAAAATATAAAAGCTACCAATCTTGTACAATTGTAATGTTAAGAATT  
TAAATAAAATTATTCCAACA

## **FIGURE 122**

MRPQGPAAASPQRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGR  
DGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK  
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMNSTINIHTS  
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

## **FIGURE 123**

GCTGAGCGTGTGCGCGTACGGGCTCTGCCTCTGGCTCCAACGCAGCTCTGGCTGAA  
CTGGGTGCTCATCACGGGAACTGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCCTGGAAGAATACATCATGTTTCGATAAGAAGAAATTGTTAGGATCCAGTTTTTTTA  
ACCGCCCCCTCCCCACCCCCAAAAAAACTGTAAGATGCAAAAACGTAATATCCATGAAGATCC  
TATTACCTAGGAAGATTGATTTGCTGCGAATGGGTGTTGGGATTATTGTTCTGGAG  
TGTTCGGTGGCTGGCAAGAATAATGTTCAAATCGGTCCATCTCCAAAGGGGTCCAATT  
TCTTCCTGGTGTAGCGAGGCTGACTACAGTCAGCTGACAGGGCTGTCATGCAACTG  
GCCCTAAAGCCAAAGCAGGACTAAGGACGACTTGAACAATAACAAAGGATGGGTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGAGCACTGGTTATAGCCCCACTGTTACTGACAATG  
CTTCTCTGCCGAACGAGGATGCCCTAAGGGCTGAGGTGAAGGCAAATGGTATATTGTA  
ATCTCAGAAATTACAGGAGATACTCTCAAGTATATCTGGTGTAGTTGTCCTTCGCT  
ATAACAGCCTCAAAACTTAAGTATACTAATTAAAGGGCTCAACAGCTCACGGTATAC  
CTTGACCCATAACCATATCAGCAATATTGAGGAAATGCTTTAATGGAATACGAGACTAAGA  
GCTGATTCTTAGTCCAATAGAATCTCTATTCTTACAATACCTTCAGACCTGTGACAATT  
TACGGAACCTGGATCTGCTCTATAATCAGCTGATTCTGGGATCTGACAGCTTCGGGCTTG  
CGGAAGCTGCTGAGTTACATTACGGCTAACTCCCTGAGAACCATCCCTGCGAATT  
AGACTGCCAACCTGGAACCTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATG  
TCTTGGTGGCATGATCAGACTCAAAGAACCTCACCTGGAGCACAATCAATTTCAGCTCAAC  
CTGGCCCTTTCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCAGTGGATAAAATCAGTGT  
CATAGGACAGACCATGTCCTGGACCTGGAGCTCCTACAAAGGCTGATTATCAGGCAATGAGA  
TCGAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCGAATCTGCAGGCCCTCACCTGGAT  
TCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCTCAATGACATCAG  
TCTTGCTGGGAATATATGGGAATGAGCAGAAATATTGCTCCCTGAAACTGGCTAAAAGTT  
TTAAAGGTCAAGGGAGAATACAATTATCTGTCAGTCCAAAGAGCTGCAAGGAGTAAATGTG  
ATCGATGCAAGAACCTACAGCATCTGGCAAAAGTACTACAGAGAGGTTGATCTGGCAG  
GGCTCTCCAAAGCCGACGTTAACGCCAACGACTCCCCAGGCCGAAGCATGAGAGCAAACCCCTT  
TGCCCCCGACGGTGGGAGCCACAGAGCCGGCAGAGACCGATGCTGACGCCAGCACATCT  
TTCCATAAAATCATCGGGGAGCGTGGCCTTCTGTCGTGCTCATCTGCTGGTTAT  
CTACGTGTCATGGAAGCGGTACCCCTGCGAGCATGAGCAGCTGCAAGCAGCGCTCCCTCATGCGAA  
GGCACAGGAAAAGAAAAGACAGTCCCTAACGCAAATGACTCCCAGCACCCAGGAATT  
GATTATAAACCCACCAACCGGAGACCAGCGAGATGCTGAACTGGGACGGACCCCTGCAACCTA  
TAACAAATGGGCTCCAGGGAGTGTGAGGTATGAAACCATTGTGATAAAAAGAGCTTAAAAGCT  
GGGAAATAAGTGGTGTCTTATTGAACTCTGGTACTATCAAGGGAACCGCAGTGGCCCTCC  
TCCCTCTCCCTCACTTGGTGGCAAGATCCTCTGTCGTTAGTGCATTCAATAACT  
GGTCATTCTCTCATACATAATCAACCCATTGAAATTAAATACCAATCAATGTGAAGCTT  
GAACTCCGGTTAATATAACCTATTGATAAGACCCCTTACTGATTCCATTAAATGTCGCAATT  
GTTTAAGATAAAACTCTTCTAGTAAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMYCSESQKLQEIPSSISAGCLG  
LSLRYNLSQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNNTFR  
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKELHLEHNQFSKLNLAFLPRLVSLQNLQWNKISVIGQTMSTWSSLQRLDL  
SGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLFIGQEILDWSWISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDIARALPKPTFKPKLPRKHE  
SKPPLPPTVGATEPGPETDADAEHISFKIIAGSVALFLSVLVIILVIYVSWKRYPASMKQLQQR  
SLMRRHRKKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## **FIGURE 125**

CCGTTATCGTCTTGCCTACTGCTGAATGTCGTCCGCTCCGGAGGAGGGAGGGCTTTGCCGCTG  
ACCCAGAGATGGCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGCGCTACCGTGGCCGAGCT  
AGCAACCTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTTTGCTC  
GGTGGGAGACGGTGAAGAGAACTGCCCCTAGGGGAATGGTGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCATTACAGACACGTAGT  
GTATTCTGGAGGTCAATGGTCACATATGAACATCTCGAGAGGTGTGTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTT  
TTAGCCAATCCAACTGACCTAGTGAAGGTTCAGATGCAATGGAAAGGAAAACTGGAAGG  
AAAACCATTGCGATTCTGTGGTGTACATCATGCATTGCAAAATCTAGCTGAAGGAGGAATAC  
GAGGGCTTGGCAGGCTGGTACCAATATAACAAAGAGCAGCACTGGTGAATATGGAGATTAA  
ACCACTTATGATAACAGTGAAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC  
TCACGGTTATCAAGTTATGTTCTGGACTGGTAGCTCTATTCTGGAACACCAGCCATGTCA  
TCAAAAGCAGAATAATGAATCAACCACGAGATAAAACAAGGAAGGGACTTTTGATAAATCATCG  
ACTGACTGCTTGATTCAGGCTGGTCAAGGTGAAGGATTCATGAGTCTATATAAAAGGCTTTTAC  
ATCTTGGCTGAGAATGACCCCTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGARES  
APYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMOMEGRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTPADVIKSrimnQP  
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## **FIGURE 127**

CGCGGATCGGACCAAGCAGGTGGCGGCCGGCAGGAGAGCGGCCGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGCGTGGGCCATGGCCAGGCCGGCATGG  
AGCGGTGGCGCACCGCTGGCGCTGGTACGGGGGCTCGGGGGCATCGGCCGGCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGCTGCGCCCGACTGTGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTCAGGCTACCCGGACTTGATCCCCTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGAGACATC  
TGCATCAACAATGCTGGCTTGGCCCGGCCTGACACCCCTGCTCTCAGGCAGCACAGTGGTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGAAAGCCTACCAGTCCATGA  
AGGAGCGGAATGTGGACGATGGCACATCATTAACATCAATAGCATGTCGCCACCGAGTGTGTTA  
CCCCTGCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTACTGCCGTGACAGAGGGACT  
GAGGCAAGAGCTCGGGAGGCCAGACCCACATCCGAGGCCACGTGCATCTCTCCAGGTGTGGTGG  
AGACACAATTGCCCTCAAACCTCCACGACAAGGACCTGAGAAGGCAGCTGCCACCTATGACCAA  
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCCCTCAGCACCCCCGCACA  
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGACTGTGGAGCTCC  
TCCTTCCCTCCCCACCCCTCATGGCTGCCCTGCCTCTGGATTTAGGTGTTGAGTTCTGGAT  
CACGGGATACCACTCCTGTCCACACCCGACCAGGGCTAGAAAATTGTTGAGATTTATA  
TCATCTGTCAAATTGCTCAGTTGAAATGTGAAAAATGGGCTGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTACTTGTAACTTGTCTTGTGCCCTGGGACTTGGCTTGTGCTCTCAGTG  
TCTTCCCTTGACATGGGAAAGGAGTTGTGGCCAAATCCCCATCTTGTGACCTCAACGTCTG  
TGGCTCAGGGCTGGGTGGCAGAGGGAGGCCTCACCTTATCTGTGTTGTTATCCAGGGCTCC  
AGACTTCCCTCTGCCCTGCCCCACTGCACCCCTCTCCCCCTATCTATCTCCTCTCGGCTCCCC  
AGCCCAAGTCTGGCTTGTCCCCCTGGGGTACCCCTCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCTGGCCCAGTGGATTCATGGTGATCATTAAAAAGAAAAATCGAACCAA  
AAAAAA

## **FIGURE 128**

MARPGMERWRDRRLALVTGASGGIGAAVARALVQQGLKVVGCARTVGNIEELAAECKSAGYPGTLI  
PYRCDLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNLALSICTR  
EAYQSMKERNVDDGHIININSMGHRVLPLSVTHFYSATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMCKLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## **FIGURE 129**

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTCCTCAGCCTCCTGCCGGTGGCCTACACCAT  
CATGTCCCTCCCACCCCTCCTTGACTGCGGGCCGTTCAAGGTGCAAGAGTCTCAGTTGCCCGGGAGC  
ACCTCCCTCCCAGGGCAGTCTGCTCAGAGGGCCTCGGCCAGAATTCCAGTTCTGGTTCATGC  
CAGCCTGTAAGGGCATGGAACTTGGGTGAATCACCGATGCCATTAAAGAGGGTTTCTGCCA  
GGATGGAATGTTAGGTCGTTCTGTCTGCGCTGTTCAATTTCAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTGAAATGAGGAACTGAGAAAATTAAATTCTCATGTATTTCATTTATTAA  
TTAATTAACTGATAGTTGACATATTGGGGTACATGTGATATTGGATACTGTATACAA  
TATATAATGATCAAATCAGGGTAACGGGATATCCATCACATCAAACATTATTATTATTCTTT  
TTAGACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTAGCTGGACTACAGGCAT  
CTCTGCTGCCAGGGTCAAGCGATTCTCATGCCCTCACCTCCAAAGTAGCTGGACTACAGGCAT  
GCACCCAAATGCCCAACTAAATTGTATTAGTAGAGACGGGGTTTGCCTGTTGCCAG  
CTGGCCTGAACCTGGCCTCAAACAATCCACTTGCCCTGGCCTCCAAAGTGTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCTAAACATTATCTTGTGTTGGAACTTTGAAATTAT  
ACAATGAATTATTGTTAAGTGTACATCTCCCTGCTGTGCTATGGAACACTGGACTTCTCCCTCT  
ATCTAACTGTATATTGTACCACTGACTTCATCCCCACTCCTCTATCCTTCCC  
AACCTCTGATCACCTCATTCTACTCTCACCTCCATGAGATCCACTTTAGCTCCACATGTG  
AGTAAGAAAATGCAATATTGTCTTCTGCTGGCTATTCACTAACATAATGACTCCCTG  
TTCCATCCATGTTGCTGCAAATGACAGGATTCGTTCTAATTCAATTAAATAACCACACATG  
GCAAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSSLRGPRPRIPLVSCQPV  
KGHGTLGESPMPPFKRVFCQDGTVRSFCVCAVHFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

## **FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGACTAAAATTGGCTGTTCTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCCTG  
TCCATCTGTGTGCGCTGCGATGCGGGTTCTATTTACTGTAATGATCGCTTCTGACATCCATTCAAACAG  
GAATACCAGAGGATGCTACAACTCTACCTTCAGAACACCAAATAATAATGCTGGGATTCCCTCAGAT  
TTGAAAAACTTGTGAAAGTAGAAAGAATATAACCTATAACCACAAACAGTTAGATGAATTCCCTACCAACCT  
CCCAAAGTATGTAAGAGTTACATTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTCAA  
AAATTCCCTATCTGGAAGAATTACATTAGATGACAACCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCCGACTGCTTTCTGTCCCGTAATCACCTAGCACAATTCCCTGGGTTT  
GCCAGGACTATAGAAGAACTACCGCTGGATGATAATCGCATATCCACTATTCATCACCATCTTCAAG  
GTCTCACTAGTCTAAAACGCCTGGTCTAGATGAAACCTGTTGAACAATCATGGTTAGGTGACAAGTT  
TTCTTCACCTAGTTAATTGACAGAGCTGTCCTGGTGCAGAATTCCCTGACTGCTGCACAGTAACCT  
TCCAGGCACAAACCTGAGGAAGCTTATCTCAAGATAACCACATCAATCGGGTCCCCAAATGTTTT  
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCATAATAACCTAAGTAATTACCTCAGGGTATCTT  
GATGATTGGACAATATAACACAACGATTCTCGCAACAATCCCTGGTATTGCGGGTGCAGATGAAATG  
GGTACGTGACTGGTACAATCACTACCTGTGAAGGTCAACGTGCGTGGCTCATGTGCCAAGCCCCAGAAA  
AGGTTGGTGGATGGCTATTAGGATCTCAATGCAGAACTGTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTCAAGATAACCACGTGCAATACCCAAACACAGTGTATCCTGCCAAGGACAGTGGCAGCTCAGTGAC  
CAAACAGCCAGATATTAAGAACCCCAAGCTCAACTAGGATCAACAAACACAGGGAGTCCCTCAAGAAAAAA  
CAATTACAATTACTGTGAAGTCTGTCACCTCTGATACCATTCTATCTCTGGAAACTTGCTCTACCTATG  
ACTGTTGAGACTCAGCTGGCTAAACTGGCCATAGGCCGGCATTTGGATCTATAACAGAAACAATTGT  
AACAGGGGAAACGCACTGAGTACTTGGTCACAGCCCTGGAGGCTGATTCAACCTATAAAAGTATGCTGGT  
CCATGGAAACAGCAACCTCTACCTATTGATGAAACTCCTGTTGATTGAGACTGAAACTGCACCCCTT  
CGAATGTACAACCCCTACAACCACCCCTCAATCGAGAGCAAGAGAAGAACCTTACAAAACCCAAATTAC  
TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTCCTGTTGCTTAGTGTGGTATG  
TTCATAGGAATGGATCGCTTCTCAAGGAACGTGCAATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAAGCTGGCACTAAGAAGGACAACCTATCCTGGAAATCAGGGAAACTCTTTCAGATGTTACCAAT  
AAGCAATGAACCCATCTCGAAGGAGGAGTTGTAACACACCATATTCCCTCTAATGGAATGAATCTGT  
ACAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTGGGTTAAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL  
EELHLDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL  
QGLTSKLRLVLDGNLLNNHGLGDKVFFNVLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGI FDDLDNITQLILRNNPWYCGCKMKWVRDWLQLSPV  
KVNVRGLMCQAPEKVRGMAIKDNLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTQPD  
IKNPKLTKDQQTGSPSRKTITITVKSVDTSIHIISWKLALPMTAHLRLSWLKGHS PAFGSITET  
IVTGERSEYLVTALEPDSPYKVCVMVPMETSNLYLFDETPVCIETETAPLRMYNPTTLLNREQEKE  
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS  
ILEIRETSFQMLPISNEPISKEEVIHTIFPPNGMNLYKNNHSESSSNRSYRDSGIPDSDHSHS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,  
640-645

**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

### **FIGURE 133**

CCGTCATCCCCCTGCAGCCACCCCTCCCAGAGTCCTTGCAGGCCACCCAGGCTTCTGGCA  
GCCCTGCCGGGCCACTTGTCTTCATGTCTGCCAGGGGAGGTGGGAAGGAGGTGGAGGGCG  
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGTGAGCGTGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGCTGCTGCTCTGCTTACTGACAGCACTGCCACCGCTGTGGT  
CCTCCTCACTGCCTGGCTGGACACTGCTGAAAGTAAAGCCACCATTCAGACACTGATCCTGTCT  
GCGCTGGAGAGAGGCCACCGTCTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGGTCCGAGTGTGGAAAGAGCAGCTAAAAGTGTCCGGGAGAAGTGGGCCAGGAGCCCCCTGC  
TGCAGCCGCTGAGCCTGCGCTGGGATGCTGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGTACCTAACAGAGGTTCCAGCTGACCCCTCCAGCCGG  
GTTTGAAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTGGTGTACCCCACGTTGGGC  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGTACGCTGCGCTGGTGCAGCTGCTGGGAACCGGGACG  
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCGGCTGCTC  
AGGCTACTGCCTGTCACCAACTGCTCTTCTCCTGGGCCAGAATGAGGGGATGCACACAGG  
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTGCGCCAACATGATGGACTTGAACCGC  
AGAGCTGAGGCCATCGGATACGCCAACCTTACCCGGACATCTTCATGGAAAACATCATGTTCTG  
TGGAAATGGCGGCTCTCGACTTCTACAAGCTCCGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTCGGGAGCCTGATGCTGAAAGATGAAAGATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTCGAGGGAGGTGAAGAGGCAGAAAAACAATTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTGCCTCCTGGTTCAAGC  
AATTCTCTGCCTCATCCTCCCCAGTAGCTGGACTACAGGAGCGTGCACCCATACCTGGCTAAT  
TTTATATTTTTAGAGACAGGGTTCATGTTGCTCATGCTGGCTCGAACCTCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTGGGATTATAGGTGAGGCCACCGTGTCTG  
GCTGAAAAGCACTTCAAAGAGACTGTGTTGAATAAGGGCAAGGTTCTGCCACCCAGCACTC  
ATGGGGCTCTCCCTAGATGGCTGCTCTCCACAACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTCCTATACATCCTGGCAGAATACCCCCCAGCAAACAGAGAGGCCACACCCATCCACACCG  
CCACCAAGCAGCCGCTGAGACGGACGGTCCATGCCAGCTGCCGGAGGAGGAACAGACCC  
TTTAGCTCATCCCTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCCAACTTGGAAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAGTCAACTGCAACTGAAAAAAAAAAAA

## **FIGURE 134**

MSARGRWEGGRRACRGSGLARAQGAERVTSSERPMASLGLLLLLTLPPPLWSSSLPGLD  
TAESKATIADLILSALERATVFQRLPEINLDGMGVVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD  
YINLFCANMMDLNRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSWQKQQEGCFG  
EPDAEDEELSKAIQYQQHFSRRVKREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFQFSCLILP  
SSWDYRSVPYLANFYIFLVETGFHHVAHAGLELLISRDPPSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

## **FIGURE 135**

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTCCCGCCTGCTGCTG  
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTCAAGATTGAGGGCGTGCAGTTGTTCCAGGGGTGAAGC  
CTCAGGACTGGATCTCGCGGCCGAGTGTGGTAGACGGAGAACGACGTGGTTCCAGGGTAAAG  
ACAGATGGGAGTTGTGGTTCATGATATACTCTGGATCTTATGAGTGGAAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCGTGTGGATATCACTCGAAAGGAAATGAGAGCAAGATATG  
TGAATTACATCAAAACATCAGAGGTTGTCAAGACTGCCCTATCCTCTCAAATGAAATCTCAGGT  
CCACCTTCTTACTTTATTAAAGGAATCGTGGGCTGGACAGACTTCTAATGAACCCAAATGGT  
TATGATGATGGTTCTCCTTATTGATATTGTGCTCTGCCTAAAGTGGTCAACACAAGTGTAC  
CTGACATGAGACGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTCTCTCAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAACAGGCAAAGTGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTGCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTGGAAAACCGTGTGAAGCAACTACTATAAACTT  
GAGTCATCCCGACGTTGATCTTACAACGTGTATGTT  
AACTTTTAGCACATGTTGTACTTGGTACACGAGAAAACCCAGCTTCATCTTGTCTGTAT  
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT  
ATGAACTACTATACTATTATGATATTAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLSDVQSSEVPGAAEGSGSGVGIGDRFKIEGRAVPGVKPQDWISAA  
RVLVDGEEHVGFLLKTDGSFVVHDIPSGSYVVEVVSPAYRFDPVRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPVMVMMVPLLI FVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSGSSKTGKSGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## **FIGURE 137**

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCGATTCTCCCCAGTTCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTCTGGAAAGGGAGGCATATGCGTCATTCCCCAAACAA  
GTTTGACATTCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC  
CTTACCTGCTGGGACTAACGGCGAGCCAGGATGGGACAGAATAAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACCTAGACCTGAAATCTCTTCACGGGAGGCTGGCAGT  
TTTCTACTCCTGTTGCTCCAGATTCAGGCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC  
CTTCTCTGCTGCGTTTATCTCTATGGACTCCTCCACTGGACTGAAGACACTCAATTGGG  
AAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATGGATTCTGAGATAACGGGCAGTG  
TGCAAGCCAAGATGGAAACATTGACATCAGAATCTAAGGAGGACTGAGTCTTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCTCCTGCCATTGCTAAGACTCTATCTGGACAGGGTATTAA  
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAAGATCAGCAGCCTCGCCAATTCTTCTA  
CCATCAAGAAGGACCTCCGGCTCTCATGCCACATGACATGCCATTGTGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTCTGAGTCACTTGAAAAGCTGGAAACCTCAGGCAGCAGTGTGAAGGC  
TTTGGGGAACTAGACATTCTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTG  
CTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCTCAATACCTGCAAGAGGAGGATGACCCCA  
ACCACCATCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTGCATTACTG  
CTTCCTGCAATTGCTTTATGCATCCCCATCTTAATTGAGACCATCTGTATAAGATTT  
TGTAATATCTTCTGCTATTGGATATATTATTAGTTAATATTTATTGCTATT  
ATGTATTATTTTACTTGGACATGAAACTTAAAAAAATTCAAGATTATTTATAACCTG  
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAAAAACCTTGTAAATTCTAGAAGAGTGG  
CTAGGGGGTTATTCAATTGCTTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGAT  
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGGAATAAGTTTGATGTGGAATTGCAC  
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCATAATTGTGTATCTCCAG  
CCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAGTTCTTGCATACCAAAAAAAA  
AAAAAAAAAAA

## **FIGURE 138**

MRQFPKTSFDISPMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF  
SSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS  
SLANSFLTICKDLRLSHAHMTCHC GEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET  
E

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

## **FIGURE 139**

CCGGAGCCGAAGCGCGCTGCAGCAGGGCGAGGCTCCAGGTGGGTCGGTCCGCATCCAGCC  
TAGCGTGTCCACGATCGGGCTGGGCTCCGGGACTTCTCCGCTACCTGTGCGTAGCGATCGAGGTGC  
TAGGGATCGCGGTCTTCCTCGGGGATTCTTCCCGGCTCCGGTCCGGTCCGTTCTCTGCCAGAGCGGAA  
CACGGAGCGGAGCCCCCAGCGCCGAACCTCGGCTGGAGCCAGTCTTAACCTGACCACGCTGCC  
ACCACCTCTCTTCACTAAAGTGTATTGTTCTGATAGATGCTTAGAGAGATGATTTGTGTTG  
GGTCAAAGGGTGTGAAATTATGCCCTACACAACCTTACCTGTGAAAAGGAGCATCTCACAGT  
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCCTCGAATCAAGGCATTGATGACGGGGAG  
CCTTCCGGCTTGTGACGTCATCAGGAACCTCAATTCTCCTGCAGTGGAAAGACAGTGTGA  
TAAGACAAGCAAAAAGCAGCTGGAAAAGAATAGTCTTTATGGAGATGAAACCTGGGTTAAATTA  
TTCCCAAGCATTGTGGAATTATGATGGAACACCTCATTTTCTGTGAGATTACACAGAGGT  
GGATAATAATGTACAGGGATTGGATAAAAGTATTAAAAGAGGGAGATTGGGACATATTAATCC  
TCCACTACCTGGGCTGGCACCATTTGCCACATTCAAGGGCCAAACAGCCCCCTGATTGGCAG  
AAGCTGAGCAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA  
GACGCCCTAACCAATTGCTGGTTCTTGTGGTACCATGGCATGTGAAACAGGAAGTCACG  
GGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTAACTCAGTTCTGCGTTGAAAGGAAA  
CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACTGCGATAGC  
ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTATTCCCACTGTGGAAGGAAGAC  
CAATGAGAGAGCAGTTGAGATTTCACATTGAATACAGTCAGCTTAGTAAACTGTTGCAAGAG  
AATGTGCCGTATGAAAAAGATCTGGGTTGAGCAGTTAAATGTCAAGAAAGATTGCAATGG  
GAACCTGGATCAGACTGTACTGGAGGAAAGCATTGAGAAGCTCTATTCAACCTGGCTCCAAGG  
TTCTCAGGCACTGGATGCTCTGAAAGACGCTGAGCTGTCCTGAGTGCAAGTGCAACTGGCCAG  
TTCTCACCCCTGCTCTGTCAGCGTCCCACAGGCACTGCAAGAAAGGCTGAGCTGGAAGTCCC  
CTGTCATCTGGGTTCTGCTCTTTATTGGTATCCTGGTCTTCCGGCGTTCACT  
CATTGTGTGCACCTCAGCTGAAAGTCTGCTACTCTGTGGCCTCTGTTGGCTGGCGCAGGCT  
GCCTTCGTTACCAAGACTCTGGTTGAAACACCTGGTGTGAGCAGTGTGGCAGTGCCCTGG  
AGGGGCTCAGGAAGGACGTGGAGCAGCCTTATCCCAAGGCTCTGGGTGTCCCACACAGGT  
TTCACATCTGTGCTGTCAGATGCTCAGTTCTGGAAAGCTAGGTTCTGCACTGTTAC  
CAAGGTGATTGTAAGAGACTGGCGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGAA  
TCGGACAGCCTCCCAGCAGAGGTGTGGAGCAGCTGAGGGAAGAAGAGACAATCGGCTGG  
CACTCAGGAGGGTCAAAAGGAGACTTGGTCGCACCACTCATCCTGCCACCCCCAGAATGCA  
GCCTCATCAGGTCCAGATTCTTCAAGGGCGACGTTCTGTTGGAATTCTTAGTCCTGGCC  
TCGGACACCTCATCGTTAGCTGGGAGTGGTGGTGGAGGGCAGTGAAGAAGAGGGGAGATGGTCAC  
ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCACTGGCAGCAGGACTGTTGGCCCC  
ACCCCAACCTGCACAGCCCTCATCCCTTGGCTTGGAGCAGTGGCAGAGGCTGTGCTGAGTGT  
CTGACCGAGACACTCACAGTTGTCACTCAGGGCACAGGCTCTGGAGGCCAGGATGATCTGT  
CCACGCTTGACCTCGGGCCATCTGGCTCATGCTCTCTCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGTAGTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFFAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF  
SKVVIVLIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDSVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFVSDYTEVDNNV  
TRHLDKVLKRGDWDLILYLHHLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHTSLOSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites.**

amino acids 56-60, 194-198

**N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site.**

amino acids 154-158

**Cell attachment sequence.**

amino acids 205-208

## **FIGURE 141**

GGCACGAGGCAAGCCTTCCAGGTATCGTGACGCACCTGAAAGTCTGAGAGCTACTGCCCTACA  
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAACT  
TCCCTATAGAAAACAACGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC  
CCGAAGAAATTCAGCATTCATGACCAGGATCACAAAGTACTGGTCTGGACTCTGGGAATCTCAT  
AGCAGTTCCAGATAAAAACTACATACGCCAGAGATCTTCTTGCATTAGCCTCATCCTTGAGCT  
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGCTCTAAAGGGAGTTTGCTCTAC  
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTCAGCTGAAGAAGGAGAAACTGATGAAGCT  
GGCTGCCAAAAGGAATCAGCACGCCGCCCTCATCTTATAGGGCTCAGGTGGCTCCTGGA  
ACATGCTGGAGTCGGCGCTCACCCGGATGGTCATCTGCACCTCCTGCAATTGTAATGAGCCT  
GTTGGGTGACAGATAAATTGAGAACAGGAAACACATTGAATTTCATTCACCAGTTGCAA  
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAACTGCCCATTAGAACGCCTTCCCTCGCTA  
ATTTGAACTAATTGTATAAAAACACCAAACTGCTCACT

## **FIGURE 142**

MLLLLLEYNFPPIENNQHLKTTHTFRVKNLNPKKFSIHQDHKVLVLDGNLIAVPDKNYIRPEI  
FFALASSLSSASAEGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFI  
FYRAQVGWSNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 33-36

**N-myristoylation site.**  
amino acids 50-55, 87-92

**Interleukin-1**  
amino acids 37-182

## **FIGURE 143**

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTAA  
TCCAGGATCCTGTCCTCCTGTCCTGTTAGGAGTGCCTGTCAGTGTGGGGTGGAGACAAGTTG  
TCCCACAGGGCTGTCGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACTCCTGTGGG  
CACGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG  
AAGGGAGGTCTGTCCTGGCGCTGCTGCTGCTCTCTAGGCTCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTGCTGTCACACATTCAACCAACAGAGCAAGGACTACTATGCCACAGACTGGGG  
CACATCTTGAATTCCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGAAATTGAAGACGACATTGACAACGCCATTCCAAGAAAGCACAG  
AGCTGAACAATACTTTACCTGCTTCTTCACCATCAGCACCCAGGCCCTGGATGACTCAGTTCA  
CTCCTGAACAAGACCTGCTGGAGGGATTCCACTGAGTGAAACCCACTCACAGGCTTGCCATGT  
GCTGCTCCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT  
TTGGACTTGTGTTATCCTATTTGCATGTGTTGAGATCTCAGATCAGTGTGTTAGAAAATCC  
ACACATCTTGAACCTAATCATGTAGTGTAGATCATTAAACATCAGCATTAAAGAAAAAAAAAAAA  
AAA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP  
WMTQFSLLNKTCLEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristoylation site.**

amino acids 9-15

## **FIGURE 145**

CTGTGCAGCTCGAGGGCTCCAGAGGCACACTCCAGAGAGGCCAAGGTTCTGACCGGATGAGGAAG  
CACCTGAGCTGGTGGCTGGCACTGTCTGCATGCTGCTCTGCACCCACCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAACATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA  
CTGAGGGCCCAGGTGGCTGAGAACCGCCGGGAGCCTCATCAAGCAAGGCCGCAAGCTGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA  
CTACAACGGCTGCTTGAGGCTAATGTGACCAAGGAGGCATTGTCACCGGCTGCATCAATGCCA  
CCCAGGGCGGAACCAAGGGGGAGTCCAGAACAGAACAGCTCCACCAGCAGGTGCTGG  
CGGCTGGTCCAGGGAGCTCTGCTCCCTCAAGCATTGCGAGTTGGTGGAGAGGGCGCAGGACT  
TCGGGTACCAGTCACCAGCCAGTGCCTCTGCCTCTGGCTTGATCTGGCTATGGTGAAAT  
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCGAGCAAATCTGGCAAGTGACCCAGCT  
CTTCTCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGGGATGCACTCGCACTGCCAA  
TGCGCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCCTGATAGATGGGGACTGTGGCTCT  
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTG  
GAGAAGAACACATCAGGCACTGCGCCACCTGCTCACAGTACTTCCAACAACTCTAGAGGTAG  
GTGTATTCCCCTTACAGATAAGGAAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCTGGCTGTCTAACCCAGGTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTATGTCACTTATGTCTCACAGGGACCACATCCAACATGTAT  
CTCTAAATGAAATTGTGAAAGCTCCATGTTAGAAATAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSWWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAVTGCINATQAANQGEFQKPDNKLHQQ  
VLWRLVQELCSLKHCFWLERGAGLRTMHQPVLLCLLALIWLVMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

## **FIGURE 147**

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGCGTGACCAACCATGTCGGTCCAGAGTCATTT  
CCTGATGATTATAGACTCAAAGAAAACTCATGTTCAGAAGCTCTCTCTCTGGCCTCCTCT  
CTGTCTTCTTCCCTTTCTTATTAAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTCATTTGCTGTCAGGGTAGGTCAGTGGGTTAGGTCACTGAGTCTTAGTTTATTTTGAATTT  
CAACTTCAGATTCAAGGGGTACATGTGAAGGTTGTTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLILISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

### FIGURE 149

GTCTCCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGACTTGAC  
TCCCGCGGCCCAACCTGCTTATCCCTGACCGTCAGGTGTCAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCCGCCCCACACCCACCCCTCTGGCTTCTCTGGAGACTCCTCCTTTCAATTCTA  
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGCTGTGACCCAAGGCCAGCGTGGAGAAGAATGGGTT  
CCTCGGGACCGGCACTGGATTCTGGTTAGTGCTCCGATTCAAGCTTCCCCAACCTGGAGGAA  
GCCAAGACAAATCTCTACATAATAGAGAATTAAAGTGCAAGAAAGACCTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAAAACATATCCTCCAGAAAACAAGCCAGGTAGAGCAACTATTCTT  
TGTTGATAACCTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAATTGAGAAAGAAGACAATCTA  
TAAGAACGCTCCCCACTTGATAATAAGTTGAATGTGAAGATGTTGATTCAACCAAGAACATGAAAATG  
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTCAAGATGATCCAGATGGTCTTC  
TCAACTAGACGGGACTCCTTAACCGCTGAAGACATTGTCATAAAATCGTGCAGGATTATGAG  
AAAATGACAGAGCCGTGTTGACAAGATTGTTCTAAACTACTTAATCTCGGCCATTACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAATTAATCTCAAAGGAAGCCAACAA  
TTATGAGGAGGATCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAAGATGGTCTGCTAAGGGAGAAACGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTGGAAAGGAGAACTAAAACCTACAGTGAGACAACTTGTAGGAACCTCA  
ATATTCCCAAATTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAGAGCAAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTGTGAAGATGATGGTGAAGACATGAAATATGGAACAAATATCT  
CCAGAAGAAGGTGTTCTACCTGAAAACCTGGATGAAATGATTGCTCTCAGACCAAAACAGCT  
AGAAAAAAATGCTACTGACAATATAAGCAAGCTTTCCAGCACCACAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAACAGAAGCCTATTGGAAGC  
CATCAGAAAAAAATTTGAATGGTGAAGAAACATGACAAAAAGGGAAATAAGAAGATTATGACCTT  
CAAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTGTGGAGAAAGGCATCCTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAAATGGCAAAAGATCCAGGAGTCTTCAA  
CTGTTCTAGAAAACATAATATAGCTTAAACACTCTAATTCTGTGATTAAGGTTAAAACATAGCTTCTTCCC  
GTTATTAGAAAGTGCTGAATTACAGTAGTTAACCTTACAAGTGGTAAAACATAGCTTCTTCCC  
GTAAAAACTATCTGAAAGTAAAGTGTATGTAAGCTGAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLPIQAFPKPGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG  
QSNYSFVDNLNLLKAITKEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDFKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPFKVTPMAAIQDGLAKGENETVSNTLTLNGLE  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNKLEKNATDNISKLFPAPEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKGKGNKEDYDLSKMRDFINKQADAYVEKGILDK  
EEAEAIIKRIYSSL

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

## **FIGURE 151**

CGGCTCGAGGCTCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCCTGIGGAGCTCAA  
GATGGTCTGAGTGGGGCGCTGTGCTTCCGATGAAGGACTCGGCATTGAAGGTCTTATCTGC  
ATAATAACCAGCTCTAGCTGGAGGGCTGCATGCAGGGAAAGGTCTTAAAGGTGAAGAGATCAGC  
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCAGGGTGAAG  
CCAGTGCCTGTCACTGTGGGTGGGGCAGGGCCACTCTAACACTAGAGCCAGTGAACATCATGG  
AGCTCTATCTTGGTGCAGGAAATCCAAGAGCTTCACCTCTACCCGGGGCATGGGCTCACC  
TCCAGCTCGAGTCGGCTGCCTACCCGGGCTGGTCTGTGCAAGGTGCTGAAGCCGATCAGCC  
TGTAGACTCACCCAGCTCCGAGAATGGTGGCTGGAATGCCCATCACAGACTTCTACTTCC  
AGCAGTGTGACTAGGGCAACGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
GAGTGGAGGGAGACCCATGGCGGACAATCACTCTCTCAGGACCCCCACGTCTGACTTAG  
TGGGCACCTGACCCTTGTCTGGTCTGGTCCAGTTGGATAAATTCTGAGATTGGAGCTCAGT  
CCACGGCTCCCCACTGGATGGTGCACTGCTGTGGAACCTGTAAAAACCATGTGGGTAAA  
CTGGGATAACATGAAAAGATTCTGTGGGGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
TAATGGTAACTGACAAGTGTACCTGAGCCCCCGCAGGCCAACCATCCCCAGTTGAGCCTATA  
GGGTAGCTCCACATGAAGTCTGTCACTCACCAGTGTGCAAGGAGAGGGAGGTGGTCATA  
GAGTCAGGGATCTATGCCCTTGGCCAGCCCCAACCCCTTCCCTTAATCTGCCACTGTCATA  
TGCTACCTTCTATCTCCCTCATCATCTTGTGTTGGGATGAGGAGGGTGGTGTAGTCAGAA  
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTAAAAACCAA  
GATACAATCAAATCCCAGATGCTGGTCTCATCCCATGAAAAGTGTCTGACATATTGAGA  
AGACCTACTTACAAAGTGGCATATAATTGCAATTATTTAATTAAAAGATACCTATTATATATT  
TCTTTATAGAAAAAAGTCTGGAAGAGTTACTCAATTGTAGCAATGTCAGGGGGGGGGGGGG  
AGGTGATTTCTTTAATTCTGTTAATTATCTGTTATTTCTCTAATTTTCTACAATGAAGATGA  
ATTCCCTGTATAAAAATAAGAAAATTAACTTGGAGGTAAGCAGAGCAGACATCATCTG  
TTGTCCTCAGCCTCCACTTCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTCTGGTTGG  
TTGTAGTAGTGTAGCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGGCTGTGCTGAGTTGT  
GTGGCTGGAACTCTGGGTAAGGAACCTAAAGAACAAAAATCATCTGTAATTCTTCTAGAAG  
GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA  
ATTGTGCCCCCTCAAATTCAACATCCTTCTTGGAAATCTCAGTGTGAGTTATTGGAGATAAG  
GTCTCTGAGATGTAGTTAGTAAAGACAAGGTATGCTGGATGAAGGTAGACCTAAATTCAATAT  
GACTGGTTCTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA  
AAGATGAAGGGCAGACATCGGAATTTCAGGCCAACAGCTAAGAAACACCAAGGATTGTGGCAACC  
ATCAGAAGCTTGGAGAGGCAAGAAGAATTCTCCCTAGAGGCTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAATCTCAGATGGCTCAGCCTCTGAAACGAAGAAGAATAAATTGGCTGTTTAA  
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCTAAATGATCCCTGT  
CTCCTCTGTTAATCTGTTGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
TAGAATATGGCAGAAGTGTGATGCCACTTCAAGATTAGGTTATAAAAGACACTGCAGCTTC  
TACTTGAGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT  
GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATGATGTTGTTTT  
AAGTTGCTCAGTTGGTCTAACCTGTTATGCAAGCAATAGATAAAATATGCAAGAGAAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEIISVVPNRWLDASLSPVILGVQGGS  
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

**N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

**Interleukin-1 signature.**

amino acids 111-131

**Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

### **FIGURE 153**

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTCTTCCTTATGGGGACCCCTGGCCACCAGCTGCCTCCTCTCTGG  
CCCTCTGGTACAGGGAGGAGCAGCTGCGCCATCAGCTCCACTGCAGGCTTGACAAGTCAAAC  
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA  
CAACACAGACGTTCGTCTCATGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTCACCTGAAGAAAGTCAGTGTGCTCCCTCAATCTGATAGGTT  
CAGCCTATATGCAGGAGGTGGTGCCTCTGGCCAGGCTCAGCAACAGGCTAACAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTATGTCTCTGAGAAAT  
GCCTGCATTTGACAGAGCAAAGCTGAAAATGAATAACTAACCCCTTCCCTGCTAGAAAATAA  
CAATTAGATGCCCAAAGCGATTTTTAACCAAAAGGAAGATGGGAAGCCAAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTGTTATA  
AGACCAGAAGGTAGACTTCTAAGCATAGATTTATTGATAACATTCACTTGTAACTGGTGTTC  
TATACACAGAAAACAATTTATTAAATAATTGTCTTTCCATAAAAAAGATTACTTCCAT  
TCCTTAGGGAAAAACCCCTAAATAGCTCATGTTCCATAATCAGTACTTTATTTATAAA  
TGTATTATTATTATAAGACTGCATTTATTATCATTTATTAAATATGGATTATT  
AGAAACATCATTGCTACTTGAGTGTAAAGGCTAATTGATATTGACAATAATT  
AGAGCTATAACATGTTATTGACCTCAATAAACACTGGATATCCC

## **FIGURE 154**

MAALQKVSSFLMGTIATSCLLLALLVQGGAAAPISHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNNTDVRILIGEKLFHGVSMERCYLMQVLNFTLEEVLFQSDRFQPYMQEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## **FIGURE 155**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCCAGCATGTACCAAGGTCACTGCAGAGGGC  
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCAAGC  
TGCCAGGTTGGGCTGGGGCAAGTGGAGTGAGAAACTGGGATCCCAGGGGAGGGTGCAGAT  
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTCTACAGGTGGTGCAT  
TCTTGGCAATGGTCATGGAACCCACACCTACAGCCACTGGCCAGCTGCTGCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGAGGTGGAGCACTGTGCTGTGCCCTCCCTAGAGCCTGCTAG  
GCCCAACCGCCACCCAGAGTCCTGTAGGGCAGTGAAGATGGACCCCTAACAGCAGGGCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTGAACCGCTCCCCCAGGACCTGTACCACGCCGT  
TGCCTGTGCCCGCACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCCGGGCAACTCGGA  
GCTGCTCTACCACAACCAGACTGTCTCTACAGGCCCATGCCATGGCGAGAAAGGGCACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTAGCTTGTGTGTGCGGCCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGCCCTTTGGAAACCTGGAGGCCAGGTGTACA  
ACCACTGCCATGAAGGGCAGGATGCCAGATGCTGGCCCTGTGAAGTGCTGTGGAGCAG  
CAGGATCCCGGGACAGGATGGGGCTTGGGAAAACCTGCACTCTGCACATTGAAAAGAG  
CAGCTGCTGCTTAGGGCCCGGAAGCTGGTGTCTGTCACTTCTCTCAGGAAAGGTTTCAA  
GTTCTGCCATTCTGGAGGCCACCACTCTGTCTCTCCCTTTCCATCCCTGCTACCTG  
GCCCAAGCACAGGCACATTCTAGATATTCCCCCTGCTGGAGAAGAAAGAGCCCTGGTTTATT  
TGTTTGTTACTCATCACTCAGTGAGCATCTTGGGTGCATTCTAGTGTAGTTACTAGTCTT  
TTGACATGGATGATTCTGAGGGAGCTGTTATTGAATGTATAGAGATTATCCAAATAAATAT  
CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGHTYSHWPSCCPKGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156

## **FIGURE 157**

CCGGCG**A**TGTCGCTCGTGCTGCTAACGCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC  
GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACACATGATCTAACATCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGACTATTCA  
ATTTGATGAATGTAAGCTGGGACTCCGGCAGATGCCAGCATCCGTTGTTGAAGGCCACCAA  
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGAGGTGCAATTACACAGGG  
CCTTCCAGACTCAGACCAAGACCCCTGGTGGTAAATGGACATTTCTACATCGGCTTCCCTGTA  
GAGCTGAACACACAGTCTATTCAATTGGGCCATAATATTCTAACATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCTGTGAATTACCTCACCAAGGCTGCTAGACCACATAATGAAATATAAAAAAA  
AGTGTGTCAAGGCCGGAACCTGTGGATCCGAACATCACTGCTTGTAAAGAAGAATGAGGAGACA  
GTAGAAGTGAACCTACAACCACTCCCTGGAAACAGATACTGGCTTATCCAACACAGCAC  
TATCATCGGTTTCTCAGGTGTTGAGCCACACCAGAAAGAAACAAACCGCAGCTTCAGTGGTGA  
TTCCAGTGACTGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTCTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTCCCT  
GGATAACAACAAAAGCAAGCCGGAGGCTGGCTGCCTCTCCTGCTGTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAAAGTGGAGGCACGAAAGGATCAAGAAGACTCC  
TCTACCACCAACTACTGCCCTTAAAGTTCTGTGGTTACCCATCTGAAATATGTTCCA  
TCACACAATTGTTACTTCACTGAATTCTCAAACCAATTGCGAGAAGTGGTACCTGCTTGAAA  
AGTGGCAGAAAAGAAAATAGCAGAGATGGTCCAGTGCAGTGGCTGCCACTAAAAGAAGGCA  
GCAGACAAAGTCGTTCTCTTCCATGACGTCAACAGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTCCCTGCTTTAACCTTCTGCA  
GTGATCTAAGAAGCCAGATTCTGACAAATACGTGGTGGTCACTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCAAGTACCACTCATGAAGGATGCCACTGCTT  
CTGTGCAGAACCTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTCCTTGT**AG**

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYSILMNVS梧  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTPIGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPTGDSSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTLLPPIKVLVVYPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVVKQQVSAGKRSQACHD  
GCCSL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-452

## **FIGURE 159**

AGCCACCAGCGAACATGACAGTGAAGACCC~~T~~GCATGCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTCTGAGTGAGGCGGCAGCTCGAAAATCCCCAAAGTAGGACATA  
CTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTGGGACCCCAACCGTACCCCTCGGAAGTTGTACAGGCCAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCATCCAGCAA  
GAGACCC~~T~~GGTCGTCGGAGGAAGCACCAAGGCTGCTGTTCTTCAGTTGGAGAAGGTGCT  
GGT~~G~~ACTGTTGGCTGCACCTGCGTCACCC~~T~~GTCATCCACCATGTGCAGTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 16O**

MTVKTLHGPAMVKYLLSILGLAFLSEAAARKIPKGHTFFQKPESCPPPGGSMKLDIGIINEN  
QRVMSMRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRLGCINAQGKEDISMNSVPIQQETLVV  
RRKHQGCSVSFQLEKVLTVGCTCVTPVIIHHVQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141

## **FIGURE 161**

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGACTCAGGACTCCAGG  
ACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCTCTGGAGGCTGAAGAGGGATT  
CAGCCCCCTGCCACCCACAGACACAGGGCTGACTGGGGTGTCTGCCCTGGCTTCTGCTG  
AGGGCCCTCAGGCCCTGGGTGCCACCTGGCACCTAGAAGATGCCCTGTGCCCTGGTCTTGC  
TGGCACTGGGCCGAAGCCCAGTGGTCTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACC  
CACTGCCTCCGGGCTCTCTGCCCTCTGGGACAGTGCACATACTCTGCCCTGCCCTGGGACAT  
CGTGCCTGCTCCGGGCCCCGTGCTGGCCTACGCACCTGCAGACAGAGCTGGTGTGAGGTGCC  
AGAAGGAGACCGACTGTGACCTGTGCTGCTGCTGCTGCACTGGCGTGCATGGGACTGG  
GAAGAGCTGAAGATGAGGAAAAGTTGGAGGAGCAGTGCACACTAGGGGTGGAGGAGCCTAGGAA  
TGGCTCTCCAGGCCAAGTCGTGCTCTCCAGGCCTACCCACTGCCCCCTGGGTCTGC  
TGGAGGTGCAAGTGCCTGCTGCCCTGTGCAAGTTGGTCAGTCTGTTGCTGTGGTATATGAC  
TGCTTCAGGCTGCCCTAGGGAGTGAAGTACGAATCTGGCTTAACTCAGCCAGGTACGAGAA  
GGAACTAACACACACAGCAGCTGCCCTGCCCTGGCTAACGTGTCAAGCAGATGGTGACA  
ACGTGCATCTGGTCTGAATGTCTTGAGGAGCAGCAGACTCGGCCCTCCCTGACTGGAATCAG  
GTCCAGGGCCCCAAAACCCGGTGGCACAAAAACCTGACTGGACCGCAGATATTACCTGAA  
CCACACAGACCTGGTCCCTGCCCTGTATTACGGTGTGGCCTGGAACCTGACTCCGTTAGGA  
CGAACATCTGCCCTTCAGGGAGGACCCCCCGCGCACACCAGAACCTCTGGCAAGCCGCCGACTG  
CGACTGCTGACCCCTGAGAGCTGGCTGCTGGACGCCGACCGTGCCTGCCCGCAGAGCGGACT  
GTGCTGGCGGGCTCCGGGTGGGACCCCTGCCAGCCACTGGTCCCACCGCTTCTGGAGAACG  
TCACTGTGGACAAGGTTCTCGAGTCCCATTGCTGAAAGGCCACCTAACCTCTGTGTTCAAGGTG  
AACAGCTGGAGAACGCTGCAGCTGCAGGAGTGTGCTGGCTGACTCCCTGGGCTCTCAAAGA  
CGATGTGCTACTGTGGAGACACGAGGCCCCCAGGACAACAGATCCCTGTGCTGGCTTGGAAACCA  
GTGGCTGACTTCACTAACCCAGCAAAGCCTCACGAGGGCAGCTGCCCTGGAGAGTACTTACTA  
CAAGACCTGCACTGAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGAGCCTATGGGCTG  
CCCCATGGACAAATACATCCACAAGCGCTGGCCCTCGTGTGGCTGGCTGCCCTACTTTGCCG  
CTGCGCTTCCCTCATCTCTCAAAAGGATACCGCAAAGGGTGGCTGAGGCTCTGAA  
CAGGACGTCCGCTCGGGCGGCCAGGGCGCAGCGCTCTGCTCTACTCAGCCGATGA  
CTCGGGTTTCGAGGCCCTGGTGGCGCCCTGGCGTCGCCCTGTGCCAGCTGCCGCTGCGCGTGG  
CCGTAGACCTGTGGAGGCCGCTGTGAACCTGAGCGCGCAGGGGCCGCTGGCTTGGTTACGCGCAG  
CGGCCGAGACCCCTGCAAGGAGGGCGGGCTGGTGGCTTGCTCTCTCCGGTGCAGGGCT  
GTGCAGCGAGTGGCTACAGGATGGGTGTCCGGGGGGGGCGCACGGCCGACGACGCCCTCC  
GCCCTCGCTCAGCTGCGTGCTGCCGACTTCTTGCAAGGGCGGGCGCCAGCTACGTGGGG  
GCCCTCGACAGGCTGCTCACCCGGACGCCGTACCCGCCCTTCCGCACCGTGCCCTCT  
CACACTGCCCTCCAACTGCCAGACTTCTGGGGCCCTGCAAGCAGCCTCGCGCCCGCTCCG  
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCAGGGCCCTTCAGCCAGCCCTGGATA  
CATCCCCGGGACTCCCGCCGGGACCGGGGACGGGACCTGGGACCTGGGGGGGGGGGGGG  
CGGGACTTAATAAAGGCAGACGCTGTTTCTAAAAAAAA

## **FIGURE 162**

MPVPWFILLSLALGRSPVVLSLERLVPQDATHCSPGLSCRILWSDSILCLPGDIVPAPGPVLAPTHLQTELVL  
LRCQKETDCDLCLRVAVHLAVHGHWEEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV  
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVS  
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNL  
LWQAARLRLLTLQSWLADAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKLEFPLLKHPNLCVQ  
VNSSEKQLQECWLADSLGPLKDDVLLLETRGPQDNRSLCALEPSGCTSILPSKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMDKYIHKRWALVWLACLLFAAALSLLKKDHAKGWRLLKQDVRSGAAARG  
RAALLLYSADDSGFERLVLGALASALCQLPLRVAVDLWSRRELSAQGPVAWFHAQRQTLQEGGVVLLFSP  
GAVALCSEWLQDGVSAGPAGHGPDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTPVVF  
LPSQLPDFL GALQQPRAPRSGRILQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
692-697, 696-701, 700-705

## **FIGURE 163**

GGGAGGGCTCTGCCCCGATGAGGACGCTGCTGACCATCTGACTGTGGGATCCCTGGCT  
GCTCACGCCCTGAGGACCCCTCGGATCTGCTCCAGCAGTCAAATTCCAGTCAGCAACTTGA  
AAACATCCTGACGTGGAGCGGGGACCCCGAGGGCACCACGGTCTACAGCATCGAGTATA  
AGACGTACGGAGAGGGACTGGGTGGCAAAGAAGGGCTGTGAGGGATCACCCGGAAAGTCTGC  
AACCTGACGGTGGAGACGGCAACCTCACGGAGCTCTACTATGCCAGGGTACCGCT  
GTCAGTGGGGAGCCGGTCAGCCACCAAGATGACTGACAGGGTCACTCTGCAGCACACTAC  
CCTCAAGCCACCTGATGTGACCTGTATCTCAAAGTGAGATCGATTAGATGATTGTCATCCTA  
CCCCCAGCAGCAATCCGTGCAGGGATGGCACCCTGAACCCCTGGAAAGACATCTCCATGACCTG  
TTCTACCAACTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAAGCAGAGAGA  
ATATGAGTTCTCGGCTGACCCCTGACACAGAGTCTTGGCACCATCATGATTGGCTTCCA  
CCTGGGCAAGGAGAGTGCCTTACATGTGCGAGTAAGACACTGCCAGACGGACATGGACC  
TACTCTTCTCGGAGCCCTCTGTTCTCCATGGGCTTCTCGCAGTACTCTGCTACCTGAG  
CTACAGATATGTCAACCAAGCCCTGCACCTCCAACTCCCTGAACGTCCAGCAGTCTGACTT  
TCCAGCCCTGCGCTCATCAGGAGCAGTCTGATCCCTGTCTTGAACCTCAGCGGCCAGC  
AGTCTGGCCAGGCTGCAAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCGCAGGAGC  
TCCACAGCGGCTAGCCTGTCGAGATCACCTACTTAGGGCAGCCAGACATCTCATCCTCAGC  
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCAAACGCTGCCCTGAG  
GTCGGGCCCCATCCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCATTCTACGCCAC  
GGCCATCTCTAAGGTCAGCCTCTCTCTATGCCCTCAAGCCACTCCGGACAGCTGGCTCCCT  
CCTATGGGGTATGCATGGAAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTCTAGTCTAAA  
CACCTTACGCCCTAAAGGTCACTTCAGAAAGGCCACAGCTGGAGCTGCATGTTAGGTGCC  
TTCTCTGCAGGAGGTGACCTCTTGGCTATGGAGGAATCCAAGAAGCAAATATTGACCC  
CCCTGGGATTGACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGAGGAAGGGACA  
CCACAGTACCTAAAGGGCCAGCTCCCCCTCTCCTCAGTCCAGATCGAGGGCCACCCATGTC  
CCTCCCTTGCAACCTCCCTCCGGTCCATGGTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGCC  
TGCTGGAGTCCCTGTGTGTCAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG  
GAGCAGCCCACAGAACTGGATCTCTTCAAGGGCTGGCCCTGACTGTGCACTGGAGTCTG  
**ATGGGAATGGGAAAGGCTTGGCTTCTCCCTGTCCCTACCCAGTGTCACTCCTTGGCTGTCA**  
ATCCCATGCCCTGCCCATGCCACACACTCTGCGATCTGCCCTCAGACGGGTGCCCTGAGAGAAGC  
AGAGGGAGTGGCATGCAGGGCCCTGCCATGGTGCCTCCCTACCCAGTGTCACTGGCC  
AGGACTGCAGGGGGAGCTCTGGGAGCAGCTGTAGACAAGCGCGTGCCTGAGCCCTG  
CAAGGCAGAAATGACAGTGCAGGGAAATGCAGGGAAACTCCCGAGGTCCAGAGCCCCACCTC  
CTAACACCATGGATCAAAGTGCCTCAGGGAAATTGCCCTCCTGGCCCTTCTGTCAATTG  
ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCCTGGCTCTGTCAATTGTTCAAGGTGG  
GCCTGGGAAAAGAACGCCCTGGAAAAGAACCAAGAGAACAGGAGGCTGGCAGAACCAAC  
ACTTCTGCCAAGGCCAGGGCAGCAGGACGGACTCTAGGGAGGGGTGTGCCCTGCAGCTCA  
TTCCCAAGGCCACTGCCCTGACGTTGACGATTTCAGCTTCAATTCTCTGTAGAACAAAGC  
GAAATGCAGGTCCACCAGGGAGGGAGACACACAAGCCTTTCTGCAGGCAGGAGTTCA  
ATCCTGAGAATGGGTTGAAAGGAAGGTGAGGGCTGTGGCCCTGGACGGTACAATAACAC  
TGTACTGATGTCAACATTGCAAGCTGCTGCCCTGGGTCAGCCCATCTGGCTCAAATTCCAGC  
CTCACCAACTCACAAGCTGTGTGACTTCAAAACAAATGAAATCAGTGCCAGAACCTCGGTT  
ATCTGTAATGTGGGGATCATAACACACTACCTCATGGAGTTGTGGTAAGATGAAATGAAGT  
TCTTAAAGTGTCTTAATAGTGCCTGGTACATGGCAGTGCCAATAACGGTAGCTATTTAAAAA  
AAAAAAA

## **FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVETGNLTEYYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTTCIS  
KVRSIQMIHVPTPTPIRGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP  
PNSLNVQRVLTFQPLRFIQEHVLIPIVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGSLQEVTLAM  
EESQEAKSLHQPLGICTDRTSDPNVLHSGEEGTPQYLKQPLLSSVQIEGHPMSPQPLQPPSGPC  
SPSDQGPSPWGLLESLVCPKDEAKSPAPETSDEQPTELDSLFRGLALTVQWES

**Signal sequence.**

amino acids 1-17

**Transmembrane domain.**

amino acids 233-250

**N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

**N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

## **FIGURE 165**

TGGCCTACTGGAAAAAAAAAAAAAAAGTCACCCGGGCCGCGGTGCCACAACATGG  
CTGCGCGCCGGGCTGCTCTCTGGCTGTTCTGGCTGGGCGCTCTGGTGGTCCCAGGCCAG  
TCGGATCTCAGCCACGGACGGCGTTCTGGACCTCAAAGTGTGCGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGAAAGCTCTGAAGACTTCACGGCCCTGATTGTCGTTGTGAATTTA  
AAAAAGGTGACGATGTATATGTCTACTACAAACTGGCAGGGGATCCCTGAACCTTGGCTGGA  
AGTGTGAACACAGTTGGATATTTCAAAGATTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTGAAGGAGGAAGAGATGATT  
TTAATAGTTATAATGTAGAAGAGCTTTAGGATCTTGGAACTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTGGGGCGTGA  
ACTTGACCTGTGCTGAGCCGAGGCATTCAAGAGCTGATTCAAGAGGATGGAGAAGGTGTTCT  
CAGAGAGCACCGAGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGGCCACCCCTCACACCAGCGGT  
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTCGTTGGACACTTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA  
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTATT  
CATTACAGCAAAGGATTCGTTGGCATAAAATCTAAGTTGTTACAAAGATTGTTTTTAGTA  
CTAAGCTGCCTTGGCAGTTGCATTTGAGCAAACAAAATATATTATTTCCCTTAAGTA  
AAAAAAAAAAAAAA

## FIGURE 166

MAAAPGLLFWLFVLGALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPDCRFVN  
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADETDFVCFEGGRD  
DFNSYNVEELLGSLELEDSPVEESKKAEEVSQHREKSPPESRGRELDPVPEPEAFRADSEDEGGA  
FSESTEGLQGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVGSERTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## **FIGURE 167**

CCAGGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAAGAGGCCGGGAAGAGAAGCAAAGCGC  
AACGGTGTGGTCCAAGCCGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAACCTC  
AGTCCCCCAAACCGCACCCTCGAAGTCTGAACTCCAGCCCGCACATCCACCGCGCGCACAGG  
CGCGGCAGGCAGGCTCCCGCGAAGGGCGATGCGCGCAGGGGCTCGGCAGCTGGGCTCGGC  
GGCAGGGAGTAGGGCCCGAGGGAGGGCAGGGCTGCATATTCAAGAGTGCAGGGCTGCGCCCTG  
GGCAGAGGCCGCCCTGCTCCACGCAACACCTGCTGCTGCCACCGCGCGCATTGAGCCGCGTGG  
TCTCGCTGCTGCTGGCGCCGCTGCTCGGCCACGGCGCTCTGCGCGCGTGGTCAGC  
GGCCAAAAGGTGTGTTGCTACTTCAGGAGGCACGCCCTGGCTGTGAGAGTGAGGGAGGAGTCCCTCA  
GTCCAGCCGAGTGAGCTTCAGGAGGCACGCCCTGGCTGTGAGAGTGAGGGAGGAGTCCCTCA  
GCCCTGAGAATGAAGCAGAACAGAAAGTTAATAGAGACATGTTGCAAAACCTGACAAAACCCGGG  
ACAGGGATTCCTGATGGTGAATTCTGGATAGGGCTTGGAGGAATGGAGATGGCAAACATCTGG  
TGCGTCCCAGATCTTACCACTGGTCTGATGGAAGCAATTCCCGTACCGAAACTGGTACACAG  
ATGAACCTCCCTGCGGAAGTGAAAAGTGTGTTGATGTATACCAACCAACTGCCAATCTGGC  
CTTGGGGGCTCCTACCTTACCACTGGTGAAGTGTGAAACATGAAGCACAATTATATTG  
CAAGTATGAACCCAGAGATTAATCCAACAGCCCTGTAAGAAAAGCCTTATCTTACAATCAACCAG  
GAGACACCCATCAGAATGTGGTGTACTGAAGCAGGTATAATTCCAATCTAATTATGTGTT  
ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTGGAACCTGTTGTTCCAGATGCT  
GCATAAAAAGTAAAGGAAGAACAAAAACTAGTCAAACCGAGTCTACACTGTGGATTCAAAGAGTA  
CCAGAAAAGTGGCATGGAAGTATAAAACTCATTGACTTGGTCCAGAATTGTAATTCT  
GGATCTGTATAAGGAATGGCATCAGAACATAGCTTGGGAATGGCTGAAATCAGGATCTGC  
AAGATGAACTGTAAGCTCCCCCTGAGGCAAATTAAAGTAATTTTATATGTCTATTATTC  
TTTAAAGAATATGCTGCTATAATGGAGTGAGACATGCTTGTGCTAAAGGATGCACCAA  
ACTTCAAACCTCAAGAACATGAAATGGACAATGCAGATAAGTTGTTATCAACACGTCGGGAGTA  
TGTGTGTTAGAAGCAATTCTTTATTCTTCACTTCACTGTTGAAATGGCTGAAATCAGGATCTGC  
TGTATATTGTATTGAAATTACAGTGTGCAAAAGTATTTCACCTTGCTATAAGTGTGTTGATAAAA  
ATGAACGTGTTCAATATTATTATTGAGACATGCTTGTGCTAAACATGCTTTGATTAAAG  
AAACTTATTACTGTGTCAGTAACTGAAATTACACACACACAAATATAGTACCATAGAAAAAGTTGT  
TTTCTCGAAATAATTCACTTTCAGCTCTGTTGGTCAATGTCTAGGAAATCTCTCAGA  
AATAAGAAGCTATTTCATTAAGTGTGATATAAACCTCTCAAACATTACTAGAGGCAAGGAT  
TGTCTAATTTCATATGTGCAAGACATGTGCTTATAATTATTAGCTTAAACAGATT  
TTGTAATAATGTAACCTTGTATAAGGTGCTAAACACTAATGCAAGTCAATTGAAACAAAAGAAG  
TGACATACACAATATAATCATATGTCCTCACACGTTGCCCTATATAATGAGAAGCAGCTCTGA  
GGGTTCTGAAATCAATGTGGCTCTCTTGGCTCACTAAACAAAGATGGTTGTTGGGGTTGGG  
ATTGACACTGGAGGCAGATAGTGCAAAAGTTAGTCTAAGGTTCCCTAGCTGTATTAGCCTCTG  
ACTATATTACTACAAAGAGGTCACTGTTGAGACAGGTGAATAGTCACTATCAGTGTGGAG  
ACAAGCACAGCACACAGACATTAGGAAGGAAAGGAACATGCAAACTGTTGAAATGGGTTGG  
AACCCATCAGTGATCGCATATTCACTGAGGTTGCTGAGATAAGGAAATGGTGGCTCTT  
CTGTTCTATCTCTAGTTCTCAATGCTTACGGCTTGTGCTTCTCAAGAGAAAGTTGTAACCT  
CTGGTCTTCATATGTCCTGTGCTCTTTAACCAATAAGAGTTGTTCTGGGGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHAFCRVVSGQKVCFADFKHPCYKMAFHELSSRVSFQEARLACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRTKTSPNQ  
STLWISKSTRKESGMEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217